

Sequence Listing

<110> Ashkenazi, Avi
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 Gao, Wei-Qiang
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 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Hillan, Kenneth J
 Kljavin, Ivar J.
 Kuo, Sophia S.
 Napier, Mary A.
 Pan, James;
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Shelton, David L.
 Stewart, Timothy A.
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				455					460					465	
Glu	Gly	Glu	Asp	Ser	Ala	Met	Thr	Asp	Met	Pro	Pro	Thr	Glu	Glu	
				470					475					480	
Val	Thr	Asp	Ile	Val	Glu	Met	Arg	Glu	Glu	Asn	Glu				
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 <211> 535
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 33, 66, 96, 387
 <223> unknown base

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 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
 ggccacatc aagaagttca ccttcgtctg catggtctg tcaactcacgc 350
 tctgtttcgt gatgttttgg acacccaacg tgtctgngaa aatcttgata 400
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcgggatcttc tcctttcttcc cagttccagt cacagtgagg gcgcatctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

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caanaaattg gggagcaggg caaacagtn acgggcagcc cacatcaaga 100

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gttttgaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgnngtg ttcctttgcg gatcttctcc 250

tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcgggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

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agac 154

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 11
 ctgatccggt tcttggtgcc cctg 24

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 <212> DNA
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 <220>
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 gctctgtcac tcacgctc 18

 <210> 13
 <211> 18
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 13
 tcatctcttc cctctccc 18

 <210> 14
 <211> 18
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 14
 ccttccgcca cggagttc 18

 <210> 15
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 <220>
 <223> Synthetic oligonucleotide probe

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 <210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
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<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

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<210> 18

<211> 1901

<212> DNA

<213> Homo sapiens

<400> 18

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ctctgcccc tgcatectgt gcagctgctg ccccgccagc cgcaactcca 150

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tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250

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atcgctgctg tcctgcccac ggtccaggac gccagccca actcgggtct 850

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Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	
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Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	
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Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	
				140					145					150	
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				155					160					165	
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	
				170					175					180	
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	
				185					190					195	
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	
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Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	
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Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	
				230					235					240	
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	
				245					250					255	
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	
				260					265					270	
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	
				275					280					285	
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	
				290					295					300	
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	
				305					310					315	
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	
				320					325					330	
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	
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Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met	

1.09T07-16T0650

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	365	370	375		
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr		
	380	385	390		
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met		
	395	400	405		
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met		
	410	415	420		
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp		
	425	430	435		
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu		
	440	445	450		
Leu Arg Asn Arg	Asp Phe Ser				
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<220>
<223> Synthetic oligonucleotide probe

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<210> 22
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<223> Synthetic oligonucleotide probe

<400> 22
cttcttccac ttctgcctgg 20

<210> 23
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

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<220>
<223> Synthetic oligonucleotide probe

<400> 24
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<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
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<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
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<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
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cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

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ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
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<210> 28
<211> 285
<212> PRT
<213> Homo sapiens

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Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
20 25 30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
ttcgttcatg gctggcgccg aacc 324

<210> 30
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
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gcggttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
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agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
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<210> 32
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 32
 cttgaggagc gtcagaagcg 20

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 33
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<210> 34
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 34
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<210> 35
 <211> 1819
 <212> DNA
 <213> Homo sapiens

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 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatatctt 1750
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 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
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 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30

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			35						40					45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
			50						55					60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
			65						70					75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
			80						85					90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
			95						100					105
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn
			110						115					120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn
			125						130					135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser
			140						145					150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val
			155						160					165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu
			170						175					180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp
			185						190					195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu						
			200											

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base
 <400> 37
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 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgtccaa tcataggaga atatgctgga 300

gagggttttga gatttgttgg tggcattggc ctgttnttca gttttacaga 350
gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38
<211> 566
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 27
<223> unknown base

<400> 38
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ttacaccaat gtattctaga atagtattgt cttaggaaat tgtggtttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagtctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 84-85, 206
<223> unknown base

<400> 39
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tggttggtgaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250
 ataggagaat atgc 264
 <210> 40
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 40
 acccacgtct gcgttgctgc c 21
 <210> 41
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 41
 gagaatatgc tggagagg 18
 <210> 42
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 42
 aggaatgcac taggattcgc gcgg 24
 <210> 43
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 43
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 <210> 44
 <211> 2061
 <212> DNA
 <213> Homo sapiens
 <400> 44
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gacgctgcag tgtgaggac ctgtctgcac tgaggagagc agctgccaca 150
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 agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
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 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt 1450
 ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500
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 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccctt 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctgggttgt 2050
 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45
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 20 25 30
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	
				155					160					165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	
				170					175					180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	
				185					190					195	
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	
				200					205					210	
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	
				215					220					225	
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	
				230					235					240	
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	
				245					250					255	
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	
				260					265					270	
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	
				275					280					285	
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	
				290					295					300	
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	
				305					310					315	
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	
				320					325					330	
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	
				335					340					345	
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		
				350					355						

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 tttccagcgc caattctc 18

 <210> 48
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 48
 agttcttgga ctgtgatagc cac 23

 <210> 49
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 49
 aaacttggtt gtcctcagtg gctg 24

 <210> 50
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 50
 gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

 <210> 51
 <211> 2181
 <212> DNA
 <213> Homo sapiens

 <400> 51
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 ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
 gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
 gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
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 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350

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cacgtgtgaa	gtcacctggc	agactcctga	tggcaaccaa	gtcgtgagag	500
ataagattac	tgagctccgt	gtccagaaac	tctctgtctc	caagcccaca	550
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tcagtccttg	ccttctgcat	ggccttcttc	cctgctacct	ctcttcctgg	1750
atagcccaaa	gtgtccgcct	accaacactg	gagccgctgg	gagtcactgg	1800

[illegible]

$\langle 211 \rangle$ 321

<213> Homo sapiens

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Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
20 25 30

Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
35 40 45

Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
50 55 60

Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
65 70 75

His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
80 85 90

Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
95 100 105

Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
110 115 120

Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
125 130 135

Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
140 145 150

Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
155 160 165

Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
170 175 180

Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr	185	190	195
Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	200	205	210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	215	220	225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	230	235	240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	245	250	255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	260	265	270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	275	280	285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	290	295	300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	305	310	315
Val	Tyr	Glu	Ala	Ala	Arg										320		

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 53
 tatccctcca attgagcacc ctgg 24

 <210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 54
 gtcggaagac atcccaacaa g 21

 <210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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cgataatgaa gggaaccaa aagtggatgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

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 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050
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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
				20					25					30
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
				80					85					90
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140					145					150
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155					160					165
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
				170					175					180

Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	185	190	195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly	230	235	240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu	245	250	255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val	275	280	285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
Ser	Met	Ile	Pro	Ser	Gln	Ser	Arg	Ala	Phe	Gln	Thr	Val			365	370	

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61
actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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 <211> 655
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
 20 25 30

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				35					40					45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
				50					55					60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
				65					70					75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
				80					85					90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
				95					100					105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
				110					115					120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
				125					130					135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
				140					145					150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
				155					160					165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
				200					205					210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
				215					220					225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
				245					250					255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
				260					265					270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
				275					280					285	
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	
				290					295					300	
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	
				305					310					315	
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly	

320	325	330
Pro Lys Arg Gly His 335	Pro Arg Gln Asn Leu His Lys His Phe Asp 340	345
Ile Asn Glu His 350	Pro Trp Met Ile Val Leu Phe Leu Leu Leu 355	360
Val Leu Val Val 365	Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg 370	375
Thr Leu Lys Lys 380	Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu 385	390
Lys Ala Gly Leu 395	Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu 400	405
Lys Trp Ile Tyr 410	Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys 415	420
Leu Val Ala Ala 425	Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln 430	435
Phe Leu Cys Asn 440	Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn 445	450
Gly Tyr Thr Ala 455	Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His 460	465
Trp Thr Ile Arg 470	Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser 475	480
Ala Leu Arg Gln 485	His Arg Arg Asn Asp Val Val Glu Lys Ile Arg 490	495
Gly Leu Met Glu 500	Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala 505	510
Leu Pro Met Ser 515	Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser 520	525
Pro Asn Ala Lys 530	Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro 535	540
Ser Pro Gln Asp 545	Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu 550	555
Pro Leu Leu Arg 560	Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu 565	570
Ser Arg Asn Gly 575	Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val 580	585
Leu Arg Gln Val 590	Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe 595	600
Asp Asp Met Leu 605	His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile 610	615

Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
				635					640					645
Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
				650					655					

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
 gtagcagtgc acatggggtg ttgg 24

<210> 66
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 66
 accgcacatc ctcagtctct gtcc 24

<210> 67
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 67
 acgatgatcg cgggctccct tctcctgctt ggattcotta gcaccaccac 50

<210> 68
 <211> 2412
 <212> DNA
 <213> Homo sapiens

<400> 68
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 ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200
 ataagtcctg ttgcaccaga tgcagatgct gttgctgcac agatcctgtc 250

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Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly
				125					130					135
His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr
				140					145					150
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe
				155					160					165
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys
				170					175					180
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala
				185					190					195
Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg
				200					205					210
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu
				215					220					225
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His
				230					235					240
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala
				245					250					255
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile
				260					265					270
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His
				275					280					285
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg
				290					295					300
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr
				305					310					315
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu
				320					325					330
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala
				335					340					345
Thr	Glu	Asp	Gly	Gly	Asp	Ala	Ser	Pro	Val	Leu	Asn	His	Ala	Ala
				350					355					360
Val	Pro	Leu	Ile	Ser	Asn	Lys	Ile	Cys	Asn	His	Arg	Asp	Val	Tyr
				365					370					375
Gly	Gly	Ile	Ile	Ser	Pro	Ser	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Thr
				380					385					390
Gly	Gly	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
				395					400					405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
440 445 450

Leu Lys Thr

<210> 70
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
tacacgtccc tgtggttgca gatc 24

<210> 72
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
cgttcaatgc agaaatgatc cagcctgtgt gcctgcccac ctctgaagag 50

<210> 73
<211> 3305
<212> DNA
<213> Homo sapiens

<400> 73
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attgcaacgg tcaaggctgg cttgtgccag aacggcgcg cgcgcgcac 100
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gctcagcggc ggcgcgggcy ctgcgcgagg gctccggagc tgactcgccg 200

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<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	
His	Val	Arg	Gly	Tyr	Ser	Asp	Ser	Ala	Val	Ser	Leu	Ser	Thr	Cys	125	130	135	
Ser	Gly	Leu	Arg	Gly	Leu	Ile	Val	Phe	Glu	Asn	Glu	Ser	Tyr	Val	140	145	150	
Leu	Glu	Pro	Met	Lys	Ser	Ala	Thr	Asn	Arg	Tyr	Lys	Leu	Phe	Pro	155	160	165	
Ala	Lys	Lys	Leu	Lys	Ser	Val	Arg	Gly	Ser	Cys	Gly	Ser	His	His	170	175	180	
Asn	Thr	Pro	Asn	Leu	Ala	Ala	Lys	Asn	Val	Phe	Pro	Pro	Pro	Ser	185	190	195	
Gln	Thr	Trp	Ala	Arg	Arg	His	Lys	Arg	Glu	Thr	Leu	Lys	Ala	Thr	200	205	210	

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Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile	Glu
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Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile	Arg
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Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys	Cys
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Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu	Asp
275	280		285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn	Ala
290	295		300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly	Met
305	310		315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly	Ile
320	325		330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr	Leu
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Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr	Leu
350	355		360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly	Cys
365	370		375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe	Ser
380	385		390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly	Met
395	400		405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe	Gly
410	415		420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu	Cys
425	430		435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn	Ala
440	445		450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly	Leu
455	460		465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys	Arg
470	475		480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly	Ala
485	490		495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His	Ser

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Cys Gln Asp Val	Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr			
	515	520			525
His Glu Gln Gln	Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro			
	530	535			540
Ala Pro Gly Ile	Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro			
	545	550			555
Tyr Gly Asn Cys	Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys			
	560	565			570
Glu Met Arg Asp	Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly			
	575	580			585
Ala Ser Arg Pro	Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr			
	590	595			600
Asn Ile Pro Leu	Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr			
	605	610			615
His Val Tyr Leu	Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu			
	620	625			630
Ala Gly Thr Lys	Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln			
	635	640			645
Cys Gln Asn Ile	Ser Val Phe Gly Val	His Glu Cys Ala Met Gln			
	650	655			660
Cys His Gly Arg	Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys			
	665	670			675
Glu Ala His Trp	Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly			
	680	685			690
Gly Ser Thr Asp	Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln			
	695	700			705
Glu Ala Ala Glu	Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro			
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Val Gly Ser Gln	Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile			
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 <212> DNA
 <213> Homo sapiens

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 <222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473
 <223> unknown base

 <400> 75

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	100%		
Marital status	Married	100%		
Education	High school	100%		
Occupation	Teacher	100%		
Income	1000 TL	100%		
Health status	Good	100%		
Smoking status	Non-smoker	100%		
Alcohol consumption	Non-drinker	100%		
Stress level	Low	100%		
Sleep quality	Good	100%		
Physical activity	Regular	100%		
Dietary habits	Healthy	100%		
Family size	2-3	100%		
Work hours	8-10	100%		
Compliance	High	100%		
Knowledge	Good	100%		
Attitude	Positive	100%		
Behavior	Responsible	100%		
Self-efficacy	High	100%		
Perceived barriers	Low	100%		
Perceived benefits	High	100%		
Health beliefs	Strong	100%		
Health status	Good	100%		
Quality of life	High	100%		
Satisfaction	High	100%		
Engagement	High	100%		
Participation	High	100%		
Commitment	High	100%		
Motivation	High	100%		
Self-regulation	High	100%		
Goal setting	High	100%		
Problem solving	High	100%		
Decision making	High	100%		
Communication	High	100%		
Teamwork	High	100%		
Leadership	High	100%		
Conflict resolution	High	100%		
Interpersonal skills	High	100%		
Emotional stability	High	100%		
Resilience	High	100%		
Stress management	High	100%		
Time management	High	100%		
Organization	High	100%		
Productivity	High	100%		
Efficiency	High	100%		
Effectiveness	High	100%		
Quality of work	High	100%		
Job satisfaction	High	100%		
Organizational commitment	High	100%		
Employee engagement	High	100%		
Team cohesion	High	100%		
Work-life balance	High	100%		
Overall well-being	High	100%		

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<223> Synthetic oligonucleotide probe

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<211> 18

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tacctgcacg atggggcac 18

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 <400> 79
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 <400> 81
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<212> PRT

<400> 85

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Ala Leu Leu His Leu Tyr His
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<210> 86

<212> DNA

<220>

<400> 86

<210> 87

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<210> 88

<212> DNA

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<211> 2956
<212> DNA
<213> Homo sapiens

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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

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Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala	35	40	45	
Ala	Asp	Gly	Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro	50	55	60	
His	Ser	Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	65	70	75	
Gln	Ser	Ala	Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	80	85	90	
His	Cys	Gln	Arg	Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	95	100	105	
Tyr	Asn	Ser	Met	Glu	Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	110	115	120	
Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly	125	130	135	
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys	140	145	150	
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu	155	160	165	
Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu	170	175	180	

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
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Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

<210> 91
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 91
 atgttcttcg cgccctgggtg 20

 <210> 92
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 92
 ccaagccaac acactctaca g 21

 <210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 93
 aagtggtcgc cttgtgcaac gtgc 24

 <210> 94
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 94
 ggtcaaagg gatatatcgc cac 23

 <210> 95
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 95
 gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

 <210> 96
 <211> 1016
 <212> DNA
 <213> Homo sapiens

 <400> 96
 cttttctgag gaaccacagc aatgaatggc ttgtcatcct tgcttogaag 50

 aaaccaattt atcctcctgg tactatcttct ttgtcaaatt cagagtctgg 100

 gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200
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gagaactggg tgatatggga gatcagggca atattggcaa gactggggccc 300
attgggaaga agggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350
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ctacatcgtg caggaagaga agaactacag ggaatcccta acccactgca 550
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ctcatcgctg actatgttgc caagagtggc ttctttcggg tgttcattgg 650
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cagttattgt tatccatcct ttttttctg attgtactac atttgatctg 950
agtcaacata gctagaaaat gctaaactga ggtatggagc ctccatcatc 1000
aaaaaaaaa aaaaaa 1016

<210> 97
<211> 277
<212> PRT
<213> Homo sapiens

<400> 97
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1 5 10 15
Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
20 25 30
Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
35 40 45
Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
50 55 60
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
65 70 75
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys

	80		85		90
Thr Gly Pro Ile	Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly Leu			
	95	100			105
Leu Gly Ile Pro	Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys Asp			
	110	115			120
Cys Gly Arg Tyr	Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser Ile			
	125	130			135
Ala Arg Leu Lys	Thr Ser Met Lys Phe	Val Lys Asn Val Ile Ala			
	140	145			150
Gly Ile Arg Glu	Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln Glu			
	155	160			165
Glu Lys Asn Tyr	Arg Glu Ser Leu Thr	His Cys Arg Ile Arg Gly			
	170	175			180
Gly Met Leu Ala	Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu Ile			
	185	190			195
Ala Asp Tyr Val	Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile Gly			
	200	205			210
Val Asn Asp Leu	Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp Asn			
	215	220			225
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro Ser			
	230	235			240
Asp Pro Tyr Gly	His Glu Asp Cys Val	Glu Met Leu Ser Ser Gly			
	245	250			255
Arg Trp Asn Asp	Thr Glu Cys His Leu	Thr Met Tyr Phe Val Cys			
	260	265			270
Glu Phe Ile Lys	Lys Lys Lys				
	275				

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 98
 cgctgactat gttgccaaga gtgg 24

 <210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctccatggc tgccctcctg ctgctgcccc tgctgctgtt gctacogctg 300

ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggtc cttcgagctc 400

gcgccctggc cgcggctgcc gccgaccgg aaggtcccga ggggggctgc 450

agcctggcct ggcgccctgc ggaactggcc cagcagcgcg ccgcgcacac 500

ctttctcatt cacggctcgc ggcgctttag ctactcagag gcggagcgcg 550

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ggacccgacg gcggcgacag cggcgagggg agcgctggag aaggcgagcg 650

ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtttg 700

ccggagggga cggtgccgcc agaggtggag gagccgccgc ccctctgtca 750

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gctctggttc gggctggcca aggccggcct gcgcaactgcc tttgtgcca 850

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 ggtgtccacc aggaagatgt gatctacctc gccctccac tctaccacat 1250
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 tgtcaaccag cccccgagca aggcagaacg tggccataag gtccggtctg 1450
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catggcccaa cttgtttatt gcag 2574

<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly	20	25	30	
Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45	
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60	
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75	
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90	
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105	
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120	
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135	
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150	
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165	
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180	
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195	
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210	

Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
215		220	225
Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
230		235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
245		250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
260		265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
275		280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
290		295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
305		310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp

	500		505		510
Val Thr Thr Gly	Glu Pro Ile Arg Asp	Pro Gln Gly His Cys Met			
	515	520			525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu	Leu Val Ala Pro Val Ser			
	530	535			540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu Ala			
	545	550			555
Gln Gly Lys Leu	Leu Lys Asp Val Phe	Arg Pro Gly Asp Val Phe			
	560	565			570
Phe Asn Thr Gly	Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe Leu			
	575	580			585
Arg Phe His Asp	Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly Glu			
	590	595			600
Asn Val Ala Thr	Thr Glu Val Ala Glu	Val Phe Glu Ala Leu Asp			
	605	610			615
Phe Leu Gln Glu	Val Asn Val Tyr Gly	Val Thr Val Pro Gly His			
	620	625			630
Glu Gly Arg Ala	Gly Met Ala Ala Leu	Val Leu Arg Pro Pro His			
	635	640			645
Ala Leu Asp Leu	Met Gln Leu Tyr Thr	His Val Ser Glu Asn Leu			
	650	655			660
Pro Pro Tyr Ala	Arg Pro Arg Phe Leu	Arg Leu Gln Glu Ser Leu			
	665	670			675
Ala Thr Thr Glu	Thr Phe Lys Gln Gln	Lys Val Arg Met Ala Asn			
	680	685			690
Glu Gly Phe Asp	Pro Ser Thr Leu Ser	Asp Pro Leu Tyr Val Leu			
	695	700			705
Asp Gln Ala Val	Gly Ala Tyr Leu Pro	Leu Thr Thr Ala Arg Tyr			
	710	715			720
Ser Ala Leu Leu	Ala Gly Asn Leu Arg	Ile			
	725	730			

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 104
ggagaatgtg gccacaac 18

<210> 105
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
acgcgcgcat acacactcgc tctcgtttgt ccatctccct ccggggggag 150
ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgcg 200

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cctgctccag ccctcagatc tgcccgtca gctcctgaaa attttaatac 1650

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

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tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150
tagggaccgc gcttttgctt tcaggctccc tagcagcggg gaaaaggaat 200
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<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

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Gln	Ala	Cys	Val	Cys	Pro	Gly	Lys	Met	Leu	Ala	Met	Gly	Ala	Leu
				20					25					30
Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser
				35					40					45
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala
				50					55					60
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln
				65					70					75
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp
				80					85					90
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys
				95					100					105
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro

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Ile Cys Thr Pro Ser Arg Ser Gln Phe	125	Ile Thr Gly Lys Tyr Gln	130		135
Ile His Thr Gly Leu Gln His Ser Ile	140	Ile Arg Pro Thr Gln Pro	145		150
Asn Cys Leu Pro Leu Asp Asn Ala Thr	155	Leu Pro Gln Lys Leu Lys	160		165
Glu Val Gly Tyr Ser Thr His Met Val	170	Gly Lys Trp His Leu Gly	175		180
Phe Asn Arg Lys Glu Cys Met Pro Thr	185	Arg Arg Gly Phe Asp Thr	190		195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	200	Asp Tyr Tyr Thr His Tyr	205		210
Lys Cys Asp Ser Pro Gly Met Cys Gly	215	Tyr Asp Leu Tyr Glu Asn	220		225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	230	Gly Ile Tyr Ser Thr Gln	235		240
Met Tyr Thr Gln Arg Val Gln Gln Ile	245	Leu Ala Ser His Asn Pro	250		255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	260	Tyr Gln Ala Val His Ser	265		270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	275	Glu His Tyr Arg Ser Ile	280		285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	290	Ala Met Leu Ser Cys Leu	295		300
Asp Glu Ala Ile Asn Asn Val Thr Leu	305	Ala Leu Lys Thr Tyr Gly	310		315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	320	Ser Ser Asp Asn Gly Gly	325		330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	335	Pro Leu Arg Gly Ser Lys	340		345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	350	Ala Val Gly Phe Val His	355		360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	365	Val Cys Lys Glu Leu Val	370		375
His Ile Thr Asp Trp Tyr Pro Thr Leu	380	Ile Ser Leu Ala Glu Gly	385		390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	395	Gly Tyr Asp Ile Trp Glu	400		405

Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His
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Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln
				425					430					435
Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 115
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 <210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 116
 ctctctgagt gtacatctgt gtgg 24

 <210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <220>
 <221> unsure
 <222> 33
 <223> unknown base

Demographics		Neurological		Psychiatric		Medical		Surgical		Other			
Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value		
Age (mean)	55.2	Gender (male/female)	32/18	Education (years)	12.5	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (range)	45-75	Gender (male/female)	32/18	Education (range)	8-18	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (SD)	8.5	Gender (male/female)	32/18	Education (SD)	2.5	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (median)	52.5	Gender (male/female)	32/18	Education (median)	12.0	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (IQR)	48-60	Gender (male/female)	32/18	Education (IQR)	10-14	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (mean)	55.2	Gender (male/female)	32/18	Education (mean)	12.5	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (range)	45-75	Gender (male/female)	32/18	Education (range)	8-18	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (SD)	8.5	Gender (male/female)	32/18	Education (SD)	2.5	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (median)	52.5	Gender (male/female)	32/18	Education (median)	12.0	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10
Age (IQR)	48-60	Gender (male/female)	32/18	Education (IQR)	10-14	Marital status (married/divorced)	28/10	Employment (employed/unemployed)	25/15	Religious affiliation (Christian/Jewish)	30/8	Language spoken at home (English/Hebrew)	28/10

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gtaataataa 2260

<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	
				20					25					30	
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

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Phe Asn Tyr Glu	Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly				
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Gly Lys Lys Gly	Asn Glu Glu Lys				
	335				

<210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
 cctcagtggc cacatgctca tg 22

<210> 121
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ggctgcacgt atggctatcc atag 24

<210> 122
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 122
 gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123
 <211> 1199
 <212> DNA
 <213> Homo sapiens

<400> 123
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 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatgggtg 150
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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
			20					25					30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35					40					45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50					55					60	

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val
			65					70					75	

Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80										85					90				
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr					
				95					100					105					
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr					
				110					115					120					
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile					
				125					130					135					
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser					
				140					145					150					
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn					
				155					160					165					
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser					
				170					175					180					
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser					
				185					190					195					
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln					
				200					205					210					
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile					
				215					220					225					
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro					
				230					235					240					
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala					
				245					250					255					
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe					
				260					265					270					
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys					
				275					280					285					
Thr	Lys	His	Asp																

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 126
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 <212> DNA

<213> Artificial Sequence
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 <400> 126
 ctgtgaatag catcctggg 19
 <210> 127
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 <212> DNA
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 cttttcaagc cactggaggg 20
 <210> 128
 <211> 24
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 ctgtagacat ccaagctggg atcc 24
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 <210> 130
 <211> 46
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic oligonucleotide probe
 <400> 130
 acctgacgct actatgggcc gaggggcagg gacgacgccc agaattg 46
 <210> 131
 <211> 2365
 <212> DNA
 <213> Homo sapiens
 <400> 131

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 caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
 tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
 tccttggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250
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 tgttacaaaa taaaa 2365

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 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 132
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 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe
 35 40 45
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn
 50 55 60
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln
 65 70 75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	80	85	90
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	95	100	105
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	110	115	120
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	125	130	135
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	140	145	150
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	155	160	165
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	170	175	180
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	185	190	195
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	200	205	210
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	215	220	225
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	230	235	240
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	245	250	255
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	260	265	270
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	275	280	285
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	290	295	300
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	305	310	315
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly			

	365		370		375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly		
	380	385	390		
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu Leu			
	395	400	405		
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu Cys			
	410	415	420		
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly Trp			
	425	430	435		
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu Gln			
	440	445	450		
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg Leu			
	455	460	465		
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly Met			
	470	475	480		
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly Leu			
	485	490	495		
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe Leu			
	500	505	510		
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala Arg			
	515	520	525		
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val Ser			
	530	535	540		
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro Glu			
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Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr Ser			
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Cys					

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 <213> Artificial Sequence

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<210> 134
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 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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gagccaggct gggccgcgtc cctgagtccc agagtggcg cggcgcgga 100

ggggcagcct tccaccacgg ggagcccagc tgtcagcgc ctcacaggaa 150

gatgctgctg cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200

ccctgggagc actgtgttgc tgcctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgggtggc actggtgggc accgatgcca ccctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agatacaaaa cagctggtgc acagctttgc tgaggggcag 400

gaccagggca ggcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcatccc tgaggctgca gcgcgtgct gtggcgagc 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgacctgga 600

gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700

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cttgtttgat gtgcacagcg tcctgcgggt ggtgctgggt gcgaatggca 800

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 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
	35	40	45
Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
	50	55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
	65	70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
	80	85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
	95	100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
	110	115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
	125	130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
	140	145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
	155	160	165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
	170	175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
	185	190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
	200	205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
	215	220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
	230	235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
	245	250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
	260	265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
	275	280	285
Glu Asp Gln Asp	Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
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Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
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Ala

<210> 138
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 <223> Synthetic oligonucleotide probe

<400> 138
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<210> 139
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 gctgtctgtc tgtctcattg 20

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<400> 140
 ggacacagta tactgaccac 20

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<400> 141
 tgcgaaccag gcagctgtaa gtgc 24

<210> 142
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tggaagaaga ggggtggtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 143

cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

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tacgttctta aatctatgaa gtcgagggac ctttcgctgc tttttagagg 150

acttctttcc ttgcttcagc aacatgaggc ttttcttctg gaacgcggtc 200

ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250

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aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350

ggctccttat ttactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcacctcgg aggctctcaa aggttgggac cagggcttga 450

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atttaatat gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600

cattccaaga aatggatcct aatgatgact ggaaactctc taaagatgag 650

gttaaagcat atttaaagaa ggagtttgaa aaacatggtg cggtggtgaa 700

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tcacttgaga tcaggagttc aagaccagcc tggccaacat ggtgaaacct 2100
tgtctctact aaaaatacaa aaattagcca ggcgtggtgg tgcacacctg 2150
tagtcccagc tactcgggag gctgagacag gagatttgct tgaaccggg 2200
aggcggaggt tgcaagtgc caagattgtg ccactgcact ccagcctggg 2250
tgacagagca agactccatc tcaaaaaaaa aaaaaagaag cagacctaca 2300

gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr
1 5 10 15

Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 146
 ctttccttgcc ttcagcaaca tgaggc 26

 <210> 147
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 147
 gccagagca ggaggaatga tgagc 25

 <210> 148
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 148
 gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

 <210> 149
 <211> 2196
 <212> DNA
 <213> Homo sapiens

 <400> 149
 aataaagctt ccttaatggt gtatatgtct ttgaagtaca tccgtgcatt 50

 ttttttttagc atccaacccat tcttcccttg tagttctcgc cccctcaaatt 100

 caccctctcc cgtagccac cgcactaaca tctcagtcgc tgaaaatgca 150

 cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200

 tctttttctc tttggtgcc caggacgga gcatggaggt cacagtacct 250

 gccaccctca acgtcctcaa tggctctgac gccgcctgc cctgcacctt 300

 caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350

 accaggagtg caacaactgc tctgaggaga tgttcctcca gttccgcatg 400

 aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450

 agggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500

 cggaggatga ggggatttac aactgctaca tcatgaaccc cctgaccgc 550

 caccgtggcc atggcaagat ccatctgcag gtcctcatgg aagagccccc 600

tgagcgggac tccacggtgg ccgtagattgt gggtagcctcc gtcgggggct 650
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 aaaaaagagc agaagctgag cacagatgac ctgaagaccg aggaggaggg 750
 caagacggac ggtgaaggca acccggatga tggcgccaag tagtggtggtg 800
 ccggccctgc agcctcccggt gtcccgctctc ctccctctctc cgccctgtac 850
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 gacgtgtggg ccctggggag aggagagaaa gggctccac ctgccagtcc 1050
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 ggtgggcagg ggtagaggag gggccgctgt cacctgcca gtgcttgct 1150
 ggcagtggct tcagagagga cctggtgggg agggagggct ttctgtgct 1200
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 gaaacttga ggggcatgtt aaagggatga ctgtgcattc cagggcactg 1350
 acgaaaagcc agggctgcag gcaaagctgg acatgtgccc tggcccagga 1400
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 gctccaggta gggggccatg tttcccagcg gggacccacc aacagaggcc 1550
 agtttcaaag tcagctgagg ggctgagggg tggggctcca tggatgaatgc 1600
 aggttgctgc aggtctgccc ttctccatgg ggtaaccacc ctgcctggg 1650
 caggggcagc caaggctggg aaatgaggag gccatgcaca gggtagggca 1700
 gctttctttg gggcttcagt gagaactctc ccagttgccc ttggtgggg 1750
 ttccacctgg cttttggcta cagagagga agggaaagcc tgaggccggc 1800
 ataaggggag gccttggaac ctgagctgcc aatgccagcc ctgtcccatc 1850
 tgcggccacg ctactcgctc ctctcccaac aactcccttc gtggggacaa 1900
 aagtgacaat tgtaggccag gcacagtggc tcacgcctgt aatcccagca 1950
 ctttgggagg ccaaggcggg tggattacct ccatctgttt agtagaaatg 2000
 ggcaaaacc catctctact aaaaatacaa gaattagctg ggcgtggtgg 2050

cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100
 tgagccccggg aagcagaggt tgcagtgaac tgagatagtg atagtgccac 2150
 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150
 Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr
 1 5 10 15
 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met
 20 25 30
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
 35 40 45
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
 50 55 60
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
 65 70 75
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
 80 85 90
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
 95 100 105
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu
 110 115 120
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg
 125 130 135
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu
 140 145 150
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser
 155 160 165
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val
 170 175 180
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
 185 190 195
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
 200 205 210
 Asp Asp Gly Ala Lys
 215

<210> 151

<211> 524
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 103, 233
<223> unknown base

<400> 151
gttgtatatg tcctgaagta catccgtgca ttttttttag catccaacca 50
tcctcccttg tagttctcgc cccctcaaatt caccttctcc cttagccac 100
ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150
gccctgccct cagcctcacg gggctcagtc tctttttctc tttggtgcc 200
ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250
aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300
aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
ctctgaggag atgttcctcc agttccgcat gaagatcatt aacctgaagc 400
tggagcggtt tcaagaccgc gtggagttct caggggaacc cagcaagtac 450
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
caactgctac atcatgaacc cccc 524

<210> 152
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
tcacggggct catctctttt tctcttttgt gccaccagg acggagcatg 50
gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100
cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
ccctgaactg gatttaccag gagtgcaca actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcggtt 250
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300
tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350
ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cgccctgccct gcaccttcaa ctccctgctac acagtgaacc acaaacagtt 50

<210> 156
<211> 2680
<212> DNA
<213> Homo sapiens

<400> 156
tgcggcgacc gtcgtacacc atgggcctcc acctccgcc ctaccgtgtg 50
gggctgctcc cggatggcct cctgttcctc ttgtgtgtgc taatgtgtgt 100
cgcggaacca gcgctcccg cggacgtca cccccagtg gtgtgtgtcc 150
ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagt 200
gtgcactacc tctgctcaa gaagaccgaa agctacttca caatctggct 250
gaacctggaa ctgctgtgtc ctgtcatcat tgactgtgtg attgacaata 300
tcaggctggg ttacaacaaa acatccaggg ccacccagtt tcctgatggg 350
gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttcct 400
ggacccagc aaaagcagcg tgggttccta tttccacacc atggtggaga 450
gccttgtggg ctgggggtac acacgggggtg aggatgtccg aggggtccc 500

tatgactggc gccgagcccc aaatgaaaac gggccctact tcctggccct 550
 ccgcgagatg atcgaggaga tgtaccagct gtatgggggc cccgtggtgc 600
 tgggtgcccc cagtatgggc aacatgtaca cgctctactt tctgcagcgg 650
 cagccgcagg cctggaagga caagtatatc cgggccttcg tgtcactggg 700
 tgcgccctgg gggggcgtgg ccaagaccct gcgcgtcctg gcttcaggag 750
 acaacaaccg gatcccagtc atcgggcccc tgaagatccg ggagcagcag 800
 cggtcagctg tctccaccag ctggctgctg ccctacaact acacatggtc 850
 acctgagaag gtgttcgtgc agacaccac aatcaactac aactgcggg 900
 actaccgcaa gttcttcag gacatcggct ttgaagatgg ctggctcatg 950
 cggcaggaca cagaagggtt ggtggaagcc acgatgccac ctggcgtgca 1000
 gctgcactgc ctctatggta ctggcgtccc cacaccagac tccttctact 1050
 atgagagctt ccctgaccgt gaccctaaaa tctgctttgg tgacggcgat 1100
 ggtactgtga acttgaagag tgccctgcag tgccaggcct ggcagagccg 1150
 ccaggagcac caagtgttgc tgcaggagct gccaggcagc gagcacatcg 1200
 agatgctggc caacgccacc accctggcct atctgaaacg tgtgctcctt 1250
 gggccctgac tcctgtgcca caggactcct gtggctcggc cgtggacctg 1300
 ctggttggcct ctggggctgt catggcccac gcgttttgca aagtttgtga 1350
 ctcaccattc aaggccccga gtcttggaact gtgaagcatc tgccatgggg 1400
 aagtgtgtt tgttatcctt tctctgtggc agtgaagaag gaagaaatga 1450
 gagtctagac tcaagggaca ctggatggca agaattgctgc tgatggtgga 1500
 actgctgtga ccttaggact ggctccacag ggtggactgg ctgggccctg 1550
 gtcccagtcc ctgcctgggg ccatgtgtcc ccctattcct gtgggctttt 1600
 catacttgcc tactggggcc tggccccgca gccttcctat gagggatgtt 1650
 actgggctgt ggtcctgtac ccagaggctc cagggatcgg ctcttgccc 1700
 ctcggtgac ccttcccaca caccagccac agataggcct gccactggtc 1750
 atgggtagct agagctgctg gcttccctgt ggcttagctg gtggccagcc 1800
 tgactggctt cctgggcgag cctagtagct cctgcaggca ggggcagttt 1850
 gttgcgttct tcgtggttcc caggccctgg gacatctcac tccactccta 1900
 cctcccttac caccaggagc attcaagctc tggattgggc agcagatgtg 1950

ccccagatcc cgcaggctgt gttccagggg ccctgatttc ctcgatgtg 2000
ctattggccc caggactgaa gctgcctccc ttcaccctgg gactgtgggt 2050
ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100
gaaagggaat ccaaggaagc agccaaggct gctcgcagct tccctgagct 2150
gcacctcttg ctaaccccac catcacactg ccaccctgcc ctagggtctc 2200
actagtacca agtgggtcag cacagggctg aggatggggc tcctatccac 2250
cctggccagc acccagctta gtgctgggac tagcccagaa acttgaatgg 2300
gaccctgaga gagccagggg tcccctgagg ccccctagg ggctttctgt 2350
ctgccccagg gtgctccatg gatctccctg tggcagcagg catggagagt 2400
cagggctgcc ttcattggcag taggctctaa gtgggtgact ggccacaggc 2450
cgagaaaagg gtacagcctc taggtggggg tcccaaagac gccttcaggc 2500
tggaactgagc tgctctccca cagggtttct gtgcagctgg attttctctg 2550
ttgcatacat gcttggcac tgtctcccct tgttcctgag tggccccaca 2600
tggggctctg agcaggctgt atctggattc tggcaataaa agtactctgg 2650
atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157
<211> 412
<212> PRT
<213> Artificial

<400> 157
Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp
1 5 10 15
Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro
20 25 30
Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly
35 40 45
Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val
50 55 60
Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile
65 70 75
Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp
80 85 90
Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr
95 100 105
Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

110	115	120
Thr Phe Ser Leu Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val Gly	
125	130	135
Ser Tyr Phe His Thr Met Val Glu Ser	Leu Val Gly Trp Gly Tyr	
140	145	150
Thr Arg Gly Glu Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg Arg	
155	160	165
Ala Pro Asn Glu Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu Met	
170	175	180
Ile Glu Glu Met Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu Val	
185	190	195
Ala His Ser Met Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln Arg	
200	205	210
Gln Pro Gln Ala Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val Ser	
215	220	225
Leu Gly Ala Pro Trp Gly Gly Val Ala	Lys Thr Leu Arg Val Leu	
230	235	240
Ala Ser Gly Asp Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu Lys	
245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr Glu	
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	
395	400	405

Lys Arg Val Leu Leu Gly Pro
410

<210> 158
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 158
ctggggctac acacggggtg agg 23

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 159
ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttctctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
cggacgcgtg ggcgacgcg tggggcggcg gcagcggcgg cgacggcgac 50
atggagagcg gggcctacgg cgcggccaag gcgggcggct ccttcgacct 100
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tctgcatct atggtgaggg ctacagcaat 200
gccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250
ctgccgctat ggcagtgcc tgggggtgct ggccttctctg gcctcggcct 300
tcttcttggg ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350
cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450
 acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500
 ttcagcttct tttccatctt ctctgggggt gtgctggcct ccctggccta 550
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 ccaactccgga ccccaacact gcctacgcct cctacccagg tgcattctgtg 650
 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700
 ctaccagccg cccctgtgt actgagtggc ggtagcgtg ggaaggggga 750
 cagagagggc cctccctct gccctggact ttcccatcag cctcctggaa 800
 ctgccagccc ctctctttca cctgttccat cctgtgcagc tgacacacag 850
 ctaaggagcc tcatagcctg gcgggggctg gcagagccac accccaagtg 900
 cctgtgcca gagggcttca gtcagccgct cactcctcca gggcactttt 950
 aggaaagggg ttttagctag tgttttctt cgcttttaac gacctcagcc 1000
 ccgcctgcag tggctagaag ccagcaggtg cccatgtgct actgacaagt 1050
 gcctcagctt cccccggcc cggttcaggc cgtgggagcc gctattatct 1100
 gcgttctctg ccaaagactc gtggggggcca tcacacctgc cctgtgcagc 1150
 ggagccggac caggctcttg tgcctcact caggtttgct tcccctgtgc 1200
 ccaactgctgt atgatctggg ggccaccacc ctgtgccggt ggcctctggg 1250
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 tgctcccacc cctggcagca ggaagggct ttgcctgaca acaccagct 1350
 ttatgtaaatt attctgcagt tgttacttag gaagcctggg gagggcaggg 1400
 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
 tgggggagat gcccggcctg ggatgctgtt tggagacgga ataaatgttt 1500
 tctcattcaa ag 1512

<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe
 1 5 10 15
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
 20 25 30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	155	160	165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	170	175	180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	185	190	195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	200	205	210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		215	220	

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggctcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164
gtgtactgag cggcggtag 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
ctgaaggtga tggctgccct cac 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
gagccaccta ccctgctccg aggccaggcc tgcagggcct catcggccag 50
agggatgatca gtgagcagaa ggatgcccggt ggccgaggcc ccccaggtgg 100
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
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Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	
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Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	
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Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	
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Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	
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Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	
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Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	
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Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	
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Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	
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Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	
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Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	
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Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu
				320					325					330
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro
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Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His
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Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp
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Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln
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Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile
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Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly
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Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly
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Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro
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Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys
				455					460					465
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys
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Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile
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Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly
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Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe
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Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro
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Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu
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His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly
				560					565					570
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu
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Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp	
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Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met	
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Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln	
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Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu	
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Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val	
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Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val	
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Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu	Pro	Gly	
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Leu	His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly	Gly	
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Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro	
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Gln	Asp	Leu	Cys	Ser	Glu	Ala	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg	
				725					730					735	
Met	Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln	
				740					745					750	
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	Ser	Gly	Arg	
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Trp	Phe	Leu	Ala	Gly	Leu	Val	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Arg	
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Pro	Asn	Tyr	Phe	Gly	Val	Tyr	Thr	Arg	Ile	Thr	Gly	Val	Ile	Ser	
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 <213> Homo sapiens

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 caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 172
taatccagca gtgcaggccg gg 22

<210> 173
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
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<210> 174
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
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<210> 175
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<223> Synthetic oligonucleotide probe

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<210> 176
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<213> Artificial Sequence

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<210> 177
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<212> DNA
<213> Homo sapiens

<400> 177

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aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

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35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu
95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val
110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val
125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro
200 205 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser
215 220 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
230 235 240

Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
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Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
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Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
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Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
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Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
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Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 180
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 180
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<210> 181
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 181
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<210> 182

<211> 3240
<212> DNA
<213> Homo sapiens

<400> 182

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<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	
1				5				10					15	
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp
				20					25					30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro
				35					40					45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu
				50					55					60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys
				65					70					75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro
				80					85					90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu
				95					100					105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly
				110					115					120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln
				125					130					135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His
				140					145					150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys
				155					160					165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro

	170		175		180
Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr	185		190		195
Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His	200		205		210
Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp	215		220		225
Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp	230		235		240
Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro	245		250		255
Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn	260		265		270
Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val	275		280		285
Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala	290		295		300
Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys	305		310		315
Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg	320		325		330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala	335		340		345
Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His	350		355		360
Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr	365		370		375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly	380		385		390
Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg	395		400		405
Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly	410		415		420
Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr	425		430		435
Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu	440		445		450
Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys	455		460		465

Leu Tyr Ala Ile	Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro	Leu
470		475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro	Ser
485		490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu	Asp
500		505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn	Leu
515		520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly	Gly
530		535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg	Arg
545		550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr	Asn
560		565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro	Ser
575		580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala	Arg
590		595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro	Pro
605		610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro	Ala
620		625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu	Pro
635		640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val	Val Gln Ala Leu Arg	Gly
650		655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser	Pro
665		670	675
Pro Gly Pro His	Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp	Asp
680		685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro	Gly Val Trp Val Ala	Glu
695		700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		
710			

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
 ggctgtcact gtggagacac 20

 <210> 185
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 185
 gcaaggtcat tacagctg 18

 <210> 186
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 186
 agaacatagg agcagtccca ctc 23

 <210> 187
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 187
 tgcctgctgc tgcacaatct cag 23

 <210> 188
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 188
 ggctattgct tgccttggga cagaccctgt ggcttaggct ctggc 45

 <210> 189
 <211> 663
 <212> DNA
 <213> Homo sapiens

 <400> 189
 cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50

 gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

 gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
gccccgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
atttttcata ctttttatatg tactcagact tgatcgatta atgaagtgg 350
tattttggcc ttgcttgat attatcaact cactggtaac aacagtattc 400
atgctcatcg tatctgtgtt ggactgata ccagaaacca caacattgac 450
agttggtgga ggggtgtttg cacttgtagc agcagtatgc tgtcttgccg 500
acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
1				5					10					15
Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
				20					25					30
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135
Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu
				140					145					150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggg aacaacagta ttcatgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgtctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50
ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcatgggcg 100
cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150
gccgccccgc agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200
cgcggccacg aaccgcgtag ttgcgccac cccgggaccc gggacccttg 250
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300
tccccgcggy gcgcccga cttcttgcc atggtagaca acctgcaggg 350
ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450
ggaacccgcg actcctacat agacacgtac tttgacacag agaggtctag 500
cacataccgc tccaagggtt ttgacgtcac agtgaagtac acacaaggaa 550
gctggacggg cttcggttgg gaagacctcg tcaccatccc caaaggcttc 600
aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700
cacttgccaa gccatcaagt tctctggaga cttctctoga ctccctggtg 750
acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagccgg 800
cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850
gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950
aagccttaat ctggactgca gagagtataa cgagacaag gccatcgtgg 1000
acagtggcac cagctgctg cgctgcccc agaaggtgtt tgatgcggtg 1050
gtggaagctg tggccgcgc atctctgatt ccagaattct ctgatggttt 1100

ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttgg 1150
 ctacttccc taaaatctcc atctacctga gagacgagaa ctccagcagg 1200
 tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250
 ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300
 atgcgctggg gatcggtgcc acggtgatgg agggcttcta cgtcatcttc 1350
 gacagagccc agaagagggg gggcttcgca gcgagcccct gtgcagaaat 1400
 tgcaggtgct gcagtgtctg aaatttccgg gcctttctca acagaggatg 1450
 tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500
 attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1550
 aatcgtcctg ctgctgctgc cgttccgggtg tcagcgtcgc ccccgtagacc 1600
 ctgaggtcgt caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650
 atagccaggc ctgacctcaa gcaaccatga actcagctat taagaaaatc 1700
 acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750
 caccgctctt caatctctgt tctgctccca gatgccttct agattcactg 1800
 tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196
 <211> 518
 <212> PRT
 <213> Homo sapien

<400> 196
 Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln
 1 5 10 15
 Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
 20 25 30
 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
 35 40 45
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
 50 55 60
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala
 65 70 75
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg
 80 85 90
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu
 95 100 105

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
				110					115					120	
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggctc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA

<213> Homo sapiens

<400> 205

cgcctccgcc ttcgagggt gacgcgcccg ggcgccgttc caggcctgtg 50
cagggcggtat cggcagccgc ctggcgggca tccagggcgg tgcggggcct 100
gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200
ccccgccgtg cggcggcatg ggcaacctgc ggggccgcac ggccgtggtc 250
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300
ccggggagcg cgcgtggtgc tggcctgccg cagccaggag cgcggggagg 350
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ctttctgagc tctgagccac ggttgacat cctcatccac aatgccggtg 500
tcagttcctg tggccggacc cgtgaggcgt ttaacctgct gcttcgggtg 550
aaccatatcg gtccctttct gctgacacat ctgctgctgc cttgcctgaa 600
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ggggacgtct tgacttcaaa cgcttgacc gccagtggt gggctggcgg 700
caggagctgc gggcatatgc tgacactaag ctggctaata tactgtttgc 750
ccgggagctc gccaacccagc ttgaggccac tggcgtcacc tgctatgcag 800
cccaccagg gcctgtgaac tcggagctgt tcctgcgcca tgttcctgga 850
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gtgatcttga cctccgtggt tacttttctg ggccccaagc tgtgccctgg 1400

acatctcttt tcctggttga aggaataatg ggtgattatt tcttcttgag 1450
 agtgacagta accccagatg gagagatagg ggtatgctag aactgtgct 1500
 tctcggaat ttggatgtag tattttcagg cccaccctt attgattctg 1550
 atcagctctg gagcagaggc agggagtttg caatgtgatg cactgccaac 1600
 attgagaatt agtgaactga tccctttgca accgtctagc taggtagtta 1650
 aattaccccc atgttaatga agcgaatta ggctcccgag ctaagggact 1700
 cgcctagggt ctcacagtga gtaggaggag ggctgggat ctgaacccaa 1750
 gggctctgagg ccagggccga ctgccgtaag atgggtgctg agaagtgagt 1800
 cagggcaggg cagctggtat cgagggtccc catgggagta aggggacgcc 1850
 ttccgggcgg atgcagggtt ggggtcatct gtatctgaag cccctcgaa 1900
 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
1				5					10					15
Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30
Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45
Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60
Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75
Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile
				80					85					90
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe
				95					100					105
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile
				110					115					120
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe
				125					130					135
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr
				140					145					150

His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	
				155					160					165	
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	
				170					175					180	
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	
				185					190					195	
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	
				200					205					210	
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	
				215					220					225	
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	
				230					235					240	
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	
				245					250					255	
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	
				260					265					270	
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	
				275					280					285	
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	
				290					295					300	
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	
				305					310					315	
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	
				320					325					330	
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	
				335					340					345	
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	
				350					355					360	
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

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<210> 208
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<220>
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<400> 208
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<210> 209
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<212> DNA
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<223> Synthetic oligonucleotide probe

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<210> 210
<211> 3716
<212> DNA
<213> Homo sapiens

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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150
caagcctcag gccagccacc tcccaccatc cgctgggtgc tgaatgggca 200
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Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420
Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu			

530										535					540				
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp					
				545					550					555					
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser					
				560					565					570					
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu					
				575					580					585					
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp					
				590					595					600					
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu					
				605					610					615					
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln					
				620					625					630					
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu					
				635					640					645					
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser					
				650					655					660					
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala					
				665					670					675					
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg					
				680					685					690					
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr					
				695					700					705					
Gln	Ser	Gln	Gln	Thr	Gln	Pro	Pro	Val	Ala	Pro	Gln	Ala	Pro	Ser					
				710					715					720					
Ser	Ile	Leu	Leu	Pro	Ala	Ala	Pro	Ile	Pro	Ile	Leu	Ser	Pro	Cys					
				725					730					735					
Ser	Pro	Pro	Ser	Pro	Gln	Ala	Ser	Ser	Leu	Ser	Gly	Pro	Ser	Pro					
				740					745					750					
Ala	Ser	Ser	Arg	Leu	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Leu	Gly	Glu					
				755					760					765					
Asp	Gln	Asp	Ser	Val	Leu	Thr	Pro	Glu	Glu	Val	Ala	Leu	Cys	Leu					
				770					775					780					
Glu	Leu	Ser	Glu	Gly	Glu	Glu	Thr	Pro	Arg	Asn	Ser	Val	Ser	Pro					
				785					790					795					
Met	Pro	Arg	Ala	Pro	Ser	Pro	Pro	Thr	Thr	Tyr	Gly	Tyr	Ile	Ser					
				800					805					810					
Val	Pro	Thr	Ala	Ser	Glu	Phe	Thr	Asp	Met	Gly	Arg	Thr	Gly	Gly					
				815					820					825					

Gly	Val	Gly	Pro	Lys	Gly	Gly	Val	Leu	Leu	Cys	Pro	Pro	Arg	Pro	
				830					835					840	
Cys	Leu	Thr	Pro	Thr	Pro	Ser	Glu	Gly	Ser	Leu	Ala	Asn	Gly	Trp	
				845					850					855	
Gly	Ser	Ala	Ser	Glu	Asp	Asn	Ala	Ala	Ser	Ala	Arg	Ala	Ser	Leu	
				860					865					870	
Val	Ser	Ser	Ser	Asp	Gly	Ser	Phe	Leu	Ala	Asp	Ala	His	Phe	Ala	
				875					880					885	
Arg	Ala	Leu	Ala	Val	Ala	Val	Asp	Ser	Phe	Gly	Phe	Gly	Leu	Glu	
				890					895					900	
Pro	Arg	Glu	Ala	Asp	Cys	Val	Phe	Ile	Asp	Ala	Ser	Ser	Pro	Pro	
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Ser	Pro	Arg	Asp	Glu	Ile	Phe	Leu	Thr	Pro	Asn	Leu	Ser	Leu	Pro	
				920					925					930	
Leu	Trp	Glu	Trp	Arg	Pro	Asp	Trp	Leu	Glu	Asp	Met	Glu	Val	Ser	
				935					940					945	
His	Thr	Gln	Arg	Leu	Gly	Arg	Gly	Met	Pro	Pro	Trp	Pro	Pro	Asp	
				950					955					960	
Ser	Gln	Ile	Ser	Ser	Gln	Arg	Ser	Gln	Leu	His	Cys	Arg	Met	Pro	
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Lys	Ala	Gly	Ala	Ser	Pro	Val	Asp	Tyr	Ser						
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

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 gaagggacct acatgtgtgt ggcc 24

 <210> 213
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 213
 actgaccttc cagctgagcc acac 24

 <210> 214
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

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<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

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<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly	20	25	30	
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp	35	40	45	
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg	50	55	60	
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met	65	70	75	
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	80	85	90	
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	95	100	105	
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120	
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	125	130	135	
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	155	160	165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro				

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Ala Gly Ser Ser	Arg Pro Pro Met Gln	Leu Asp Ser Thr Ser	Ala		
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Glu Asp Thr Ser	Pro Ala Leu Ser Ser	Gly Ser Ser Lys Pro	Arg		
	230	235	240		
Val Ser Ile Pro	Met Val Arg Ile Leu	Ala Pro Val Leu Val	Leu		
	245	250	255		
Leu Ser Leu Leu	Ser Ala Ala Gly Leu	Ile Ala Phe Cys Ser	His		
	260	265	270		
Leu Leu Leu Trp	Arg Lys Glu Ala Gln	Gln Ala Thr Glu Thr	Gln		
	275	280	285		
Arg Asn Glu Lys	Phe Trp Leu Ser Arg	Leu Thr Ala Glu Glu	Lys		
	290	295	300		
Glu Ala Pro Ser	Gln Ala Pro Glu Gly	Asp Val Ile Ser Met	Pro		
	305	310	315		
Pro Leu His Thr	Ser Glu Glu Glu Leu	Gly Phe Ser Lys Phe	Val		
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Ser Ala					

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 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

<400> 217
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<210> 218
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 218
 ctgtcttccc ctgcttggct gtgg 24

<210> 219
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 219
 ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
 <211> 950
 <212> DNA
 <213> Homo sapiens

<400> 220
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 ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtga 100
 cagtgtgaaa gaaccagtgg tctcgctctg ttgcccaggc tagagtgtac 150
 tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
 ctctgcctt agcctcctgc atatctggga ctccaggggt gcaactcaagc 250
 cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300
 gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
 ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgcccc 400
 gctgggatca tgttggtggc cctggtctgt ctgctcagct gcctgctacc 450
 ctccagttag gccaaactct acggtcgttg tgaactggcc agagtgtctac 500
 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggagggt 650
 ggtgcagcaa cctcaccccg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
 1 5 10 15
 Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
 20 25 30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe				
				140					145					

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 222
 gggatcatgt tggtggccct ggctc 24

<210> 223
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 223
 gcaaggcaga cccagtcagc cag 23

<210> 224
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 224
 ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccggggccggg cgcccgcggc ggcacccatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccc 100
cgagcaactg gctgtacctg gccaaagctgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc cgcggtgccc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctctt ggcaaggtgg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400
ttgcagtgcg gcgggctgac agcagtgggg agctggagaa gtgcggctgt 450
gacaggacag tgcatggggc cagcccacag ggcttcaggt ggtcaggatg 500
ctctgacaac atcgctacgc gtgtggcctt ctacagtcg tttgtggatg 550
tgcgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc caccgggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgcg cagggtgggtc acgcactgaa ggagaagttt 750
gatggtgcca ctgaggtgga gccacgccgc gtgggctcct ccagggcact 800
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850
acttgagacc tagcccccgc ttctgtgagc aggacatgcg cagcggcgtg 900
ctgggcacga ggggcccgcac atgcaacaag acgtccaagg ccatcgacgg 950
ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000
tggctgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200
ctggttttgt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300
ctgccactga ccaaagggac cttgctcgtg ccgctggctg cccgcatgtg 1350

gctgccactg accactcagt tggttatctgt gtccgttttt ctacttgacg 1400
 acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450
 gtcatacgggg aagaggggggc cttatggcag ggaaaatagg taccgacttg 1500
 atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550
 tacacatgga ctcctggcag cttgagccta gaagccatgt ctctcaaagt 1600
 ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650
 tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700
 gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750
 ccagcctgc ccagcctgc ccctgggaag aggaaactta accactcccc 1800
 agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccg 1850
 gctgtgcctt tgcagtcag cccgagtcac ctttcacagc gctgttcctc 1900
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000
 ctgtgccttt gcagtcagtc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 228
tgggtgggaga ctgttttaa at tatcggcc 28

<210> 229
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 229
tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230
<211> 1355
<212> DNA
<213> Homo sapiens

<400> 230
cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150
aggagacccc tcttcttggc cctggctgtc ctgggtcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350
ctcggggacg caggcgacg tgcagaccac gcgcgcggag cttggggagg 400
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
cgcgtgaccc agggcttggc tgaagccggc aggggccgtg aggacgtccg 500
cactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550
gcgagccgtg cccacgtcg tggctgtcct tcgagggctc ctgctacttt 600
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650
tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700
tcactcgga cagcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000
gctgctcacc tccttggtct ctggagctga ttgccaaga gtttttttct 1050
tcctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100
tgtccagccc agtgcctggg ctctgggacc tccatgccga cctcatccta 1150
actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
aaaaa 1355

<210> 231
<211> 293
<212> PRT
<213> Homo sapiens

<400> 231
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
1 5 10 15
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
20 25 30
Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
35 40 45
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
50 55 60
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
65 70 75
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
80 85 90
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
95 100 105
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
110 115 120
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	
				140					145					150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	
				155					160					165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
				170					175					180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	
				185					190					195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	
				200					205					210	
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	
				215					220					225	
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	
				230					235					240	
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	
				245					250					255	
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	
				260					265					270	
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	
				275					280					285	
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								
				290											

<210> 232
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 gcgagaactg tgtcatgatg ctgc 24

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 233
 gtttctgaga ctcagcagcg gtgg 24

<210> 234
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggggtgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctcctttt 100

ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccgggcg ccggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgtcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tcccaagca 450

gtacccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgccgt ccccagcggc accgggcaga cgtcggcgga gctggagggtg 700

cagcgcaggc actcgctggt ctcgtttggt gtgcgcacgc tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca ccttctcctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950

actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggctgcgac agagccccag ggccttcac cctcccgccc cagtccctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccgc 1100

tggactgcga ggtctccctg tggctcgtcct ggggactgtg cggaggccac 1150
 tgtgggagggc tcgggaccaa gagcaggact cgctacgtcc ggggccagcc 1200
 cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250
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 cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
 aaacagcctc ctcttttccc aaccttgctt cttagggggc cccgtgtccc 1500
 gtctgtctc agcctcctcc tcctgcagga taaagtcac cccaaggctc 1550
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600
 tgtccttcat cgtccagggg cctggctccc acgtggttgc agatacctca 1650
 gacctggtgc tctaggctgt gctgagccca ctctcccgag ggcgcatcca 1700
 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys
 1 5 10 15
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly
 20 25 30
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile
 35 40 45
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr
 50 55 60
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
 65 70 75
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val
 80 85 90
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala
 95 100 105
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val

	110		115		120
His Glu Val Phe	Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly Gln			
	125	130			135
Thr Ser Ala Glu	Leu Glu Val Gln Arg	Arg His Ser Leu Val Ser			
	140	145			150
Phe Val Val Arg	Ile Val Pro Ser Pro	Asp Trp Phe Val Gly Val			
	155	160			165
Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala			
	170	175			180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly Phe			
	185	190			195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr Val			
	200	205			210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser Phe			
	215	220			225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr			
	230	235			240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala			
	245	250			255
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala Ser			
	260	265			270
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser			
	275	280			285
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys Ser			
	290	295			300
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro			
	305	310			315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys			
	320	325			330

Val

<210> 237
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 237
 cagcactgcc aggggaagag gg 22

<210> 238
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 238
 caggactcgc tacgtccg 18

 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 239
 cagccccttc tcctcctttc tccc 24

 <210> 240
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 240
 gcagttatca gggacgcact cagcc 25

 <210> 241
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 241
 ccagcgagag gcagatag 18

 <210> 242
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 242
 cggtcaccgt gtctgcggg atg 23

 <210> 243
 <211> 42
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgtcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
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cagaaatfff atccaactff gtttgaagc ttattatgac aataccatff 350
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gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900
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<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
				20					25					30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
				35					40					45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
				50					55					60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
				65					70					75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
				80					85					90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
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Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	
				110					115					120	
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	
				125					130					135	
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	
				140					145					150	
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	
				155					160					165	
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	
				170					175					180	
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	
				185					190					195	
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	
				200					205					210	
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				215					220					225	
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	
				230					235					240	
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	
				245					250					255	
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	
				260					265					270	
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	
				275					280					285	
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	
				290					295					300	
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	
				305					310					315	
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	
				320					325					330	
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	
				335					340					345	
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	
				350					355					360	
Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	
				365					370					375	
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	
				380					385					390	
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu	

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp Met	
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys	Ser Arg Lys Val Lys Asp	
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro Arg	
440	445	450
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470		

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 247
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 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 248
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<210> 249
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<220>
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<210> 250
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<220>
 <223> Synthetic oligonucleotide probe

<400> 250
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<210> 251
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<220>
 <223> Synthetic oligonucleotide probe

<400> 251
 cctctccgat taaaacgc 18

<210> 252
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<220>
 <223> Synthetic oligonucleotide probe

<400> 252
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<210> 253
 <211> 2456
 <212> DNA
 <213> Homo sapiens

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 catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150
 ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgcggggcg 200
 gaccagcaca ggcggcgttt tctccttcgg aacgggaacg tctagcaacc 250
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 actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350
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 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
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 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro			

425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val	Ser Ser Val Pro Tyr Leu	
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn	Trp Leu Leu Pro Tyr Asn	
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val	Val Glu Glu Tyr Leu Asp	
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met	Leu Arg Asn Arg Met Met	
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val	Tyr Ala Thr Leu Gln Thr	
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met	Met Gly Ile Cys Pro Ala	
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser	Thr Cys Ser Trp Ile Leu	
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 256
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257
 gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
 <211> 2764
 <212> DNA
 <213> Homo sapiens

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tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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				20					25					30
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225
Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser
				230					235					240
His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val
				245					250					255

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
				530					535					540	
Val	Lys	Phe	Gln												

<210> 260
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 260
caaagcctgc gcctggtctg tg 22

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
ttctggagcc cagaggtgc tgag 24

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

<400> 263
tgaagagtaa tagttggaat caaaagagtc aacgcaatga actggtatatt 50
actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100
caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150
ttgagagtga agcgtggctg ggtgtggaac caatTTTTTg taccagagga 200
aatgaatacg actagtcac acatcgcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgccca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcgctactgg aagggtgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
caagtgatgc tgacgatccc tcaagtggta ataattgctcg tctcctctac 600
agcttacttc aaggccagcc atatTTTTtct gttgaaccaa caacaggagt 650
cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700
taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750
acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800
atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850
ggacttctat aggaacaatc atggcatatg ataattgacat aggagagaat 900
gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950
tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaag 1000
tggattttga gcaccagaac cactacggta ttagagcaaa agttaaaaac 1050
catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100
tttcattaag atccagggtg aagatgttga tgagcctcct cttttcctcc 1150
ttccatatta tgtatttgaa gtttttgaag aaacccaca gggatcattt 1200
gtaggcgtgg tgtctgccac agaccagac aataggaaat ctcctatcag 1250
gtattctatt actaggagca aagtgttcaa tatcaatgat aatggtacaa 1300
tcactacaag taactcactg gatcgtgaaa tcagtgcctg gtacaaccta 1350
agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400
actgtatgtg caagttctta acatcaatga tcatgctcct gagttctctc 1450
aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500
cagactatca gtgcagtgga tagagatgaa tccatagaag agcaccattt 1550
ttactttaat ctatctgtag aagacactaa caattcaagt ttacaaatca 1600
tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650
aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700
tggaatcccg tcaattacaa gtacaaacac cttaccatc catgtctgtg 1750
actgtggtga cagtgggagc acacagacct gccagtacca ggagcttgtg 1800
ctttocatgg gattcaagac agaagttatc attgctattc tcatttgcac 1850
tatgatcata tttgggttta tttttttgac tttgggttta aaacaacgga 1900

gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950
 ttccaatatg atgatgaagg ggggtggagaa gaagatacag aggcctttga 2000
 tatagcagag ctgaggagta gtaccataat gcggaacgc aagactcgga 2050
 aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100
 ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150
 agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200
 cttttgaggg aacaggggtca ttagctggat ccctgagctc cttagaatca 2250
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 tcgcttttaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350
 attagggctt tttaccatca aaatttttaa aagtgctaata gtgtattcga 2400
 acccaatggg agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450
 agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500
 ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550
 tgtaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600
 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650
 ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700
 cgagaaaatt taaaggagca aaaatttgca agtcaaataa aaatgtacaa 2750
 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850
 atttaaa 2857

<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 264
 Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu
 1 5 10 15
 Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys
 20 25 30
 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
 35 40 45
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
 50 55 60

				350					355					360
Val	Glu	Asp	Val	Asp 365	Glu	Pro	Pro	Leu	Phe 370	Leu	Leu	Pro	Tyr	Tyr 375
Val	Phe	Glu	Val	Phe 380	Glu	Glu	Thr	Pro	Gln 385	Gly	Ser	Phe	Val	Gly 390
Val	Val	Ser	Ala	Thr 395	Asp	Pro	Asp	Asn	Arg 400	Lys	Ser	Pro	Ile	Arg 405
Tyr	Ser	Ile	Thr	Arg 410	Ser	Lys	Val	Phe	Asn 415	Ile	Asn	Asp	Asn	Gly 420
Thr	Ile	Thr	Thr	Ser 425	Asn	Ser	Leu	Asp	Arg 430	Glu	Ile	Ser	Ala	Trp 435
Tyr	Asn	Leu	Ser	Ile 440	Thr	Ala	Thr	Glu	Lys 445	Tyr	Asn	Ile	Glu	Gln 450
Ile	Ser	Ser	Ile	Pro 455	Leu	Tyr	Val	Gln	Val 460	Leu	Asn	Ile	Asn	Asp 465
His	Ala	Pro	Glu	Phe 470	Ser	Gln	Tyr	Tyr	Glu 475	Thr	Tyr	Val	Cys	Glu 480
Asn	Ala	Gly	Ser	Gly 485	Gln	Val	Ile	Gln	Thr 490	Ile	Ser	Ala	Val	Asp 495
Arg	Asp	Glu	Ser	Ile 500	Glu	Glu	His	His	Phe 505	Tyr	Phe	Asn	Leu	Ser 510
Val	Glu	Asp	Thr	Asn 515	Asn	Ser	Ser	Phe	Thr 520	Ile	Ile	Asp	Asn	Gln 525
Asp	Asn	Thr	Ala	Val 530	Ile	Leu	Thr	Asn	Arg 535	Thr	Gly	Phe	Asn	Leu 540
Gln	Glu	Glu	Pro	Val 545	Phe	Tyr	Ile	Ser	Ile 550	Leu	Ile	Ala	Asp	Asn 555
Gly	Ile	Pro	Ser	Leu 560	Thr	Ser	Thr	Asn	Thr 565	Leu	Thr	Ile	His	Val 570
Cys	Asp	Cys	Gly	Asp 575	Ser	Gly	Ser	Thr	Gln 580	Thr	Cys	Gln	Tyr	Gln 585
Glu	Leu	Val	Leu	Ser 590	Met	Gly	Phe	Lys	Thr 595	Glu	Val	Ile	Ile	Ala 600
Ile	Leu	Ile	Cys	Ile 605	Met	Ile	Ile	Phe	Gly 610	Phe	Ile	Phe	Leu	Thr 615
Leu	Gly	Leu	Lys	Gln 620	Arg	Arg	Lys	Gln	Ile 625	Leu	Phe	Pro	Glu	Lys 630
Ser	Glu	Asp	Phe	Arg 635	Glu	Asn	Ile	Phe	Gln 640	Tyr	Asp	Asp	Glu	Gly 645

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg
				650					655					660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser
				665					670					675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro
				680					685					690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu
				695					700					705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr
				710					715					720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser
				725					730					735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu
				740					745					750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly
				755					760					765
Ser	Ala	Val	Gln	Ser	Asn	Asn								
				770										

<210> 265
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 24, 60, 141, 226, 228, 249, 252
 <223> unknown base

<400> 265
 atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50
 gaatattttt taaaatggat agagaactgc aagatgagta ttgggtaatc 100
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgcccggc gggcgccggac 50

cccaaccccg acccagagct tctccagcgg cggcgccagcg agcagggctc 100

cccgccttaa cttcctccgc ggggccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcac ggccaacgag gggctgcagc tgttgggctt 250

cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgccctgc 300

cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gcatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccttgatg gtggttggca tcctcctggg agtgatagca 500

atctttgtgg ccaccgttgg catgaagtgt atgaagtgct tggaagacga 550

tgagggtgcag aagatgagga tggctgtcat tgggggtgag atatttcttc 600

ttgcaggctt ggctatttta gttgccacag catggtatgg caatagaatc 650
 gttcaagaat tctatgaccc tatgaccca gtcaatgcca ggtacgaatt 700
 tggtcaggct ctcttctactg gctgggctgc tgcttctctc tgccttctgg 750
 gaggtgccct acttttctgt tccctgtcccc gaaaaacaac ctcttaccga 800
 acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850
 gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
 aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000
 gttaaaatac tcagtgcata acatggctta atcttatttt atcttctttc 1050
 ctcaatatag gaggaagat ttttccattt gtattactgc ttccattga 1100
 gtaatcatac tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150
 tgtatatata catgtttttc tattaaaaat agacagtaaa atactattct 1200
 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
 atttaattcc atattgatga agatgtttat tggatatatt tctttttcgt 1300
 ccttatatac atatgtaaca gtcaaatatc atttactctt cttcattagc 1350
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 tttcaattct tcatgcgtgc ctttttcata tacttatttt attttttacc 1450
 ataatcttat agcacttgca tcgttattaa gcccttattt gttttgtgtt 1500
 tcattggtct ctatctcctg aatctaacac atttcatagc ctacatttta 1550
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 tctttctgca tgaccaaagt gataaattcc tgttgacctt ccacacaaat 1650
 ccctgtactc tgacccatag cactcttggt tgccttgaaa atatttgtcc 1700
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 atgcgtttta tatcttccta ataagggtgtg gtctgtttgt ctgaacaaag 1900
 tgctagactt tctggagtga taatctggtg acaaatatc tctctgtagc 1950
 tgtaagcaag tcaactaatc tttctacctc ttttttctat ctgccaaatt 2000
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050

tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100
tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150
acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctattt 2200
ccactgaaca aaacctacac acataccttc atgtggttca gtgccttcct 2250
ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300
gtggctcagt gccttcctct ctctaccagt ctatttccat tctttcagct 2350
gtgtctgaca tgtttggtgt ctgttccatt ttaacaactg ctcttacttt 2400
tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450
aggggtgttg cactggtgtc tggagacctg gatttgagtc ttggtgctat 2500
caatcacctg ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550
cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600
gatgttggtg ggatccagt agatagaata catgtaagtg tggttttgta 2650
atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700
gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgттаag 2747

<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu	Gly	Trp	Ile	Gly	Ala	Ile	Val	Ser	Thr	Ala	Leu	Pro	Gln	Trp
				20					25					30
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala
				35					40					45
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly
				50					55					60
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser
				65					70					75
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu
				80					85					90
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met
				95					100					105
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val
				110					115					120

Ile Gly Gly Ala	Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val	
	125	130 135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp		
	140	145 150
Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu		
	155	160 165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala		
	170	175 180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr		
	185	190 195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr		
	200	205 210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100
 ctccctatgc tggcgacaac atcgtgaccg cccagoccat gtacgagggg 150
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatgggtgt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450
 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggctctctt 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttcctg tccc 564

<210> 272
 <211> 498

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcttgctg 200
tcgcagagca cggggcagat ccagtgc aaa gtctttgact cccttgctga 250
atctgagcag cacattgcaa gcaacccgtg ccttgatggg ggttggcacc 300
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtga 350
tgaagtgcct ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcga tatttcttct tgcaggctctg gctatttttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
gggcccgacc attatccaac cgggntcaact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atggtgggtg 250
gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgacag totggctatt tnnngttgcc 400
acagcatggg atggcaatag aatcgttcaa gaattctatg accctatgac 450

cccagtcfaat gccaggtaag aatttgggtca ggctctcttc actgggtggg 500
ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550
ga 552

<210> 274
<211> 526
<212> DNA
<213> Homo sapiens
<220>
<221> unsure
<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407
<223> unknown base

<400> 274
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ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150
ccagtgcata gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccctgct cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
ttgtggccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350
caggctctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
cnnnnntct atgacctat gacccagtc aatgccaggt acgaatttgg 450
tcaggctctc ttcactgggt gggctgctgc ttctctctgc cttctgggag 500
gtgccctact ttgctgttcc tgtccc 526

<210> 275
<211> 398
<212> DNA
<213> Homo sapiens
<220>
<221> unsure
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
<223> unknown base

<400> 275
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gcagcacatt ncaagcaacc ccttgcocttg aagggtggtg ncatcccccc 100
tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	2.5	9	16
Income	15.5	10.5	5	45
Occupation	1.5	1.5	1	5
Health status	1.5	1.5	1	5
Stress level	2.5	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Depression	1.5	1.5	1	5
Anxiety	1.5	1.5	1	5
Resilience	3.5	1.5	1	5
Optimism	3.5	1.5	1	5
Self-efficacy	3.5	1.5	1	5
Hope	3.5	1.5	1	5
Meaning in life	3.5	1.5	1	5
Life purpose	3.5	1.5	1	5
Life goals	3.5	1.5	1	5
Life values	3.5	1.5	1	5
Life beliefs	3.5	1.5	1	5
Life attitudes	3.5	1.5	1	5
Life behaviors	3.5	1.5	1	5
Life habits	3.5	1.5	1	5
Life choices	3.5	1.5	1	5
Life decisions	3.5	1.5	1	5
Life actions	3.5	1.5	1	5
Life results	3.5	1.5	1	5
Life achievements	3.5	1.5	1	5
Life contributions	3.5	1.5	1	5
Life legacies	3.5	1.5	1	5
Life impacts	3.5	1.5	1	5
Life influences	3.5	1.5	1	5
Life inspirations	3.5	1.5	1	5
Life motivations	3.5	1.5	1	5
Life passions	3.5	1.5	1	5
Life interests	3.5	1.5	1	5
Life hobbies	3.5	1.5	1	5
Life sports	3.5	1.5	1	5
Life arts	3.5	1.5	1	5
Life sciences	3.5	1.5	1	5
Life technology	3.5	1.5	1	5
Life culture	3.5	1.5	1	5
Life religion	3.5	1.5	1	5
Life philosophy	3.5	1.5	1	5
Life ethics	3.5	1.5	1	5
Life politics	3.5	1.5	1	5
Life economics	3.5	1.5	1	5
Life law	3.5	1.5	1	5
Life medicine	3.5	1.5	1	5
Life education	3.5	1.5	1	5
Life environment	3.5	1.5	1	5
Life society	3.5	1.5	1	5
Life community	3.5	1.5	1	5
Life family	3.5	1.5	1	5
Life friends	3.5	1.5	1	5
Life colleagues	3.5	1.5	1	5
Life neighbors	3.5	1.5	1	5
Life strangers	3.5	1.5	1	5
Life unknown	3.5	1.5	1	5
Life future	3.5	1.5	1	5
Life past	3.5	1.5	1	5
Life present	3.5	1.5	1	5
Life time	3.5	1.5	1	5
Life space	3.5	1.5	1	5
Life matter	3.5	1.5	1	5
Life energy	3.5	1.5	1	5
Life information	3.5	1.5	1	5
Life knowledge	3.5	1.5	1	5
Life wisdom	3.5	1.5	1	5
Life understanding	3.5	1.5	1	5
Life perception	3.5	1.5	1	5
Life cognition	3.5	1.5	1	5
Life emotion	3.5	1.5	1	5
Life feeling	3.5	1.5	1	5
Life thought	3.5	1.5	1	5
Life idea	3.5	1.5	1	5
Life concept	3.5	1.5	1	5
Life theory	3.5	1.5	1	5
Life model	3.5	1.5	1	5
Life framework	3.5	1.5	1	5
Life structure	3.5	1.5	1	5
Life system	3.5	1.5	1	5
Life mechanism	3.5	1.5	1	5
Life process	3.5	1.5	1	5
Life function	3.5	1.5	1	5
Life role	3.5	1.5		

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<220>
<221> unsure
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
<223> unknown base
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<210> 277
<211> 200
<212> DNA
<213> Homo sapiens
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<400> 277
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cacagcatgg tatggcaata gaatcggtca agaattntat gaccctatga 100
ccccagtcaa tgccagggtac gaatttggtc aggctctntt cactggntgg 150
gctgctgctt ctntnngcct tntgggaggt gccctaactt gctgttcttg 200
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<210> 278
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
<223> unknown base

<400> 278
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ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150
aagtctttga ctcttgctg aatctgagca gcacattgca agcaacntg 200
ccttgatggg ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250
accgttggca tgaagtgtga tgaagtgctt ggaagacgat gaggtgcaga 300
agatgaggat ggctgtcatt gggggcgcca tatttcttct tgcaggctctg 350
gctatttttag nngccacagc atgggtatggc aatcagaccc nntcanaaac 400
tctatgaccc tatgacccca gtcaatgccca ggtacgaatt tggtcaggct 450
ctcttactg gctgggctgc tgcttctctc tgcttctgg gaggtgccct 500
actttgctgt tcctgtcccc gaaaaacaac ctcttaccoc cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcatctcgc ttctgggat ggaatcggcg 50
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgagag caccgggcag atccagtgc aagtctttga ctcttgctg 200
aatctgagca gcacattgca agcaacntg ccttgatggg ggttggcatc 250
ctctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttctgttt cctgogaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 282
ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283
<211> 2285
<212> DNA
<213> Homo sapiens

<400> 283
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tagaggaccc ccgcccgtgc cccgaccggt cccgccttt ttgtaaaact 150
taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200
ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250
ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300

ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
caacagcggga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
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aagattgcct tgtagaggta gcatgcacag gatggtaaat tggattggtg 1000
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050
aattaatgta tgatgacatc tcacaggctc tgcctttaaa ttaccctcc 1100
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
ttagaaaagt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200
ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc ccttggggag 1350
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acgtggccca ctcccgccc aggtgcttt cagtgtcttc agttctgtcc 1450
aagccatcag ctcttgga ctgatgaaca gagtcagaag cccaaaggaa 1500
ttgcactgtg gcagcatcag acgtactcgt cataagtga aggctgtgt 1550
tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttact 1600
taaagggacc aagctaaatt tgtattggtt catgtagtga agtcaaactg 1650
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatt 1700
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agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950
tgaagagtag tcagtccttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
gcgagggcac cagcagttgt ggggtggggag caaggaaga gagaaactct 2150
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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Leu	Lys	Phe	Arg	Gly	Pro	Phe	Thr	Asp	Val	Val	Thr	Thr	Asn	Leu
				20					25					30
Lys	Leu	Gly	Asn	Pro	Thr	Asp	Arg	Asn	Val	Cys	Phe	Lys	Val	Lys
				35					40					45
Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn	Ser	Gly	Ile
				50					55					60
Ile	Asp	Ala	Gly	Ala	Ser	Ile	Asn	Val	Ser	Val	Met	Leu	Gln	Pro
				65					70					75
Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met	Val
				80					85					90
Gln	Ser	Met	Phe	Ala	Pro	Thr	Asp	Thr	Ser	Asp	Met	Glu	Ala	Val
				95					100					105
Trp	Lys	Glu	Ala	Lys	Pro	Glu	Asp	Leu	Met	Asp	Ser	Lys	Leu	Arg
				110					115					120
Cys	Val	Phe	Glu	Leu	Pro	Ala	Glu	Asn	Asp	Lys	Pro	His	Asp	Val
				125					130					135
Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu	Thr
				140					145					150

Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu
155 160 165

Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val
170 175 180

Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly
185 190 195

Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala
200 205 210

Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu
215 220 225

Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys
230 235 240

Ile Ala Leu

<210> 285
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 40, 53, 68, 119, 134, 177-178, 255
<223> unknown base

<400> 285
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ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200
cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286
<211> 543
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 73, 97

<223> unknown base

<400> 286

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gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgaagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag cttaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttacttat ttaatgtatt 450
tcattctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
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<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

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cttgtagagg tagnatgcac cnggctggtg aattggattg gtggatccac 100
catatocatg ggattttaaat ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288
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 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
 actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200
 aagggaccaa gctaaatttg tattgggttca tgtagtgaag tcaaactgtt 250
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
 ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
 ttggagagtc tggcatgtg gaggtggg 428

<210> 289
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 289
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 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
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 gaaataaatg gcagtgcctt gttaacttaa agggaccaag ctaaatttgt 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598
 <223> unknown base

<400> 290
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 ttggtaggcc ttggtacatg atgctggatt acctctotta aaatgacacc 150
 cttectcgcc tgttgggtgt gcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550
 acaagggtac agttaatgct gcgtgctgct gaantctggt ggggtgaantg 600
 gtattgctg 609

<210> 291
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 291
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 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
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 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
 gcgtgctgct gaactctggt ggggtgaactg gtattgctgc tggagggctg 450
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<210> 292
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 292
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggtccca gctgcagcgt ccccgccgc ctccctcgga 100

gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgcccagg ctggagtcca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atctttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

atcttatgtg gcacttgaga aaggtaaccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcatcgaat gccagaaaaga actcccaact ccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag cagggtcagc atcttggaaca aaagggtctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgtttctaa ctgctgcccc ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850

aataaaaagtg gaggcaagaa acgtcgaggt totaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagaggggtac cagagagcat ctgcaggaga 950
gagcgaaggg tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000
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ctcagggtcc tactctaaga agaataat aggatgctgg ttgtgtatta 1900
aatgtgaaat tgcatagata aaggtagatg gttaaagcaat tagtatcaga 1950
atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
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attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
caatgtgtat tatttaaaaa tgggagaaat agtttggtct atgaaataaa 2200
cctagtttag aaatagggaa gctgagacat ttttaagatct caagttttta 2250
tttaactaat actcaaaata tggacttttc atgtatgcat aggggaagaca 2300

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 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp	
1				5					10					15	
Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His	
				20					25					30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	
				35					40					45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	
				50					55					60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	
				65					70					75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	
				80					85					90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	
				95					100					105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	
				110					115					120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	
				125					130					135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	
				140					145					150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	
				155					160					165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	
				170					175					180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	
				185					190					195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	
				200					205					210	

Ser Gly Gly Asp	Gln Arg Glu Gly Thr	Arg Glu His Leu Gln Glu	215	220	225
Arg Ala Lys Gly	Gly Arg Arg Arg Lys	Lys Ser Gly Arg Gly Gln	230	235	240
Arg Ile Ala Glu	Gly Arg Pro Ser Phe	Gln Trp Thr Arg Val Lys	245	250	255
Asn Thr His Ile	Pro Lys Gly Trp Ala	Arg Gly Gly Met Gly Asp	260	265	270
Ala Thr Leu Asp	Tyr Asp Tyr Ala Leu	Leu Glu Leu Lys Arg Ala	275	280	285
His Lys Lys Lys	Tyr Met Glu Leu Gly	Ile Ser Pro Thr Ile Lys	290	295	300
Lys Met Pro Gly	Gly Met Ile His Phe	Ser Gly Phe Asp Asn Asp	305	310	315
Arg Ala Asp Gln	Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu	320	325	330
Ser Asn Asp Leu	Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser	335	340	345
Thr Gly Ser Gly	Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys	350	355	360
Asn Trp Lys Arg	Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp	365	370	375
Val Asp Val His	Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg	380	385	390
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly	395	400	405
Asn Asp Ala Asn	Cys Ala Tyr Gly		410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcacatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcggtccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaagggaggc cttcctttca gtggacccgg gtcaagaata ccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtggttagca 50
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtogg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcttgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccatggag tgaatgtcga cgcacctgcg ggggaggggc ctctactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatcogata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggctcttag 550
atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtgggtta 600
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ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtgggt 750
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tcacttatat ctggaaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttgggg acaattctag tgtggacttc 900

cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
agatttcatt gtcaagattc gtaactcggg ctccgctgac agtacagtcc 1000
agttcatctt ctatcaaccc atcatccacc gatggaggga gacggatttc 1050
tttccttgct cagcaacctg tggaggaggt tatcagctga catcggtga 1100
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gccctgtaa gttgtaaaag cacagactgt tctatatTTg aaactgtttt 1750
gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
taagtgtaat catctacca aagctTTTTg gctctcaaat taaagattga 1850
ttagtttcaa aaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
1				5					10					15

Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30

Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45

Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr	65	70	75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala	80	85	90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe	95	100	105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser	110	115	120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala	125	130	135
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp	140	145	150
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln	155	160	165
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly	170	175	180
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln	185	190	195
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr	200	205	210
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu	215	220	225
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser	230	235	240
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp	245	250	255
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro	260	265	270
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala	275	280	285
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg	290	295	300
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly	305	310	315
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn	320	325	330
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile	335	340	345
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro			

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctgggcgggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150
 ccagcggctg cgagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaa acgcggcctgg gccgcgccac ggccgcccag 250
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 cgccgaggag gcggcgggtc agtccgccg cgagctccgc caggccgcgg 350
 agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450

gctccaggaa gagcctagggc tggatgtctt gatcaataac gcagggatct 500
 tccagtgtccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
 caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
 aatacggaga catcaatctt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750
 ggaactagcc cgccgcttag aaggcacaaa tgtaaccgtc aatgtgttgc 800
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900
 agtagaaggt gccagactt ccatttatctt ggctcttca cctgaggtag 950
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
 cccaaagcta tggatgaatc tggtgcaaga aaactctggg atatcagtga 1050
 agtgatgggt ggctgtctaa aataggaaca aggagtaaaa gagctgttta 1100
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtatcttgg agttactgaa aaattatctt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaatatct gtcagaatta agtgactcaa agtgctatcg 1400
 agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
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 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 303
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly
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 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln
 20 25 30
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr
 35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	50	55	60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	65	70	75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	80	85	90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	95	100	105
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	110	115	120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	125	130	135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	140	145	150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	155	160	165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	170	175	180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	185	190	195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	200	205	210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	215	220	225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	230	235	240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	245	250	255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	260	265	270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	275	280	285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	290	295	300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	305	310	315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	320	325	330
Met	Val	Gly	Leu	Leu	Lys												

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
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 gcaagaaaat tntgggatat cagtgaagtg atgggtngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
 actgaaaaat tttttttggg ataagagaat ttcagcaaag atgtttttaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
 tggaaattat ctgcctggct t 521

<210> 305
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 305
 ccaggaaatg ctccaggaag agcc 24

<210> 306
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 306
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 200
gggttttttac tctgttaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaacaa tgctgatggt gcttttagtaa atttttatgc 300
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca accctcaaatt tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatattt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatggt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttacia ttggattcaa 850
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa cttttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
gctttaaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	20	25	30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg
				170					175					180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe
				185					190					195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile
				200					205					210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly
				215					220					225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys
				230					235					240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu
				245					250					255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys
				260					265					270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg
				275					280					285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp
				290					295					300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro
				305					310					315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr
				320					325					330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys
				335					340					345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe
				350					355					360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala
				365					370					375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu
				380					385					390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu
				395					400					405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 36, 48
<223> unknown base

<400> 310
attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50
gagaggacna ggtgccgtg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaacca acctagccn gtcccagccg 150
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttacccgacc tcagatgctc cttctgtctc ctggtaactt 250
gggtttttac tctgttaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 313
 gtcagcgatc agtgaaagc 19

 <210> 314
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 314
 ccagaatgaa gtagctcggc 20

 <210> 315
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 315
 ccgactcaaa atgcattgtc 20

 <210> 316
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 316
 catttggcag gaattgtcc 19

 <210> 317
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 317
 ggtgctatag gccaaagg 18

 <210> 318
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttccta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtac tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggtat ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaata gtttccacat 600
 ttttgcttgt ggaaagactg ttttcatatg ttataactcag ataaagattt 650
 taaatgggtat tacgtataaa ttaatatataa atgattacct ctgggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttggc ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaaactt catggggttc ctcactgtgc atgtcgatga ttatatatgg 950
 atacattttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt ctttaagcata agtaaacaatg atataaaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt tttaatgtgt 1150
 ttttatttgt aagacattac ttattaagaa attgggttatt atgcttactg 1200
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaatata ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5					10					15
Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25					30
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40					45
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55					60
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70					75
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85					90
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100					105

Ile	Met	Asn	Ala	Asp	Ile	Leu	Ala	Tyr	Cys	Gln	Lys	Glu	Gly	Trp
				110					115					120
Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ala	Phe	Phe	Tyr	Tyr	Leu	Tyr
				125					130					135
Gly	Met	Ile	Tyr	Val	Leu	Val	Ser	Ser						
				140										

<210> 323
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 323
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
 tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100
 cttctgtgtc atgtttcttt gtgcagcaga gtgggttaca ctgggtctca 150
 atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
 tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
 tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400
 ccaaataaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
 gaatctgatc agttacttta aaaaatg 477

<210> 324
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 324
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 325
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450
caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
aactcttgct ctctcggtga tggattgct ttggatttgt tgtgcaactg 850
ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900
ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
ttctcttggt gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050
ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
caaataaagt tactcaaatc tgtg 1174

<210> 330
<211> 323
<212> PRT
<213> Homo sapiens

<400> 330
Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly
1 5 10 15
Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser
20 25 30
Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr
35 40 45
Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr
50 55 60
Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg
65 70 75
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn
80 85 90
Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser
95 100 105
Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln
110 115 120

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331
 <211> 350
 <212> DNA
 <213> Homo sapiens

<400> 331
 ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctacccctt 50
 gcacacctac cctaaggaag aggagttgta cgcatgtcag agaggttgca 100
 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaactga 150
 actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250

aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
 tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
 <211> 562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 47
 <223> unknown base

<400> 332
 cacactggcc ggatctttta gattcctttg accttgacca agggctcngga 50
 aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100
 cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150
 tgctgaccat ggccttggcc ggaggttcgg ggaccgcttc ggctgaagca 200
 tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
 gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
 agagagggtg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350
 gacttaaatc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
 ttccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
 tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
 gatggactcc gc 562

<210> 333
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 333
 acaagctgag ctgctgtgac ag 22

<210> 334
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 335

atggccttgg ccggaggttc ggggaccgct tcggctgaag 40

<210> 336

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 336

gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50

cggcccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100

agggcgacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150

gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200

gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250

cccccgaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300

ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350

ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400

tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450

gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500

ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550

ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600

tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650

attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700

gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750

accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cctttaaatc ctttggcttc tggtaagggg 850

acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900

aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100
 tagaactaag ggcttttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350
 ttgtttttaa tgctgtctgt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
 1 5 10 15
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp
 35 40 45
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
 50 55 60
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg
 65 70 75

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp		80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln		95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr		110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu		125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys		140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe		155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp		170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp		185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys		200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln		215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu		230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His		245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu		260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln		275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg		290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu		305	310	315
Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe		320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu		335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu		350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys				

365	370	375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met Asp
380	385	390
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln Thr
395	400	405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys Leu
410	415	420
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His Leu
425	430	435
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg Ile
440	445	450
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu Gln
455	460	465

Asn Ile His

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaaagacc tttaaactct ttggcttctg gtcaaggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaaat 450
 acttcatgaa atcaagtcac ttcctttgca ttttgatgag aattcatttt 500
 tttgctg 507

<210> 339
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 339
 aagctgccgg agctgcaatg 20

 <210> 340
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 340
 ttgcttctta atcctgagcg c 21

 <210> 341
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 341
 aaaggaggac ttctgactgc 20

 <210> 342
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 342
 agagattcat ccactgctcc aagtcg 26

 <210> 343
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 343
 tgtccagaaa caggcacata tcagc 25

 <210> 344
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 344
agacagcggc acagaggtgc ttctgccagg ttagtggtta ctgggatgat 50

<210> 345
<211> 1486
<212> DNA

<213> Homo sapiens

<400> 345
cggacgcgtg ggcggacgcg tggcgacgcg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150
cactcacctg ttcttgcccc tgggtgttcct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatggat 300
gctgggtggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg gggggccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agagggtggg ggcagtgtct ctgaaggctc ataaaagaaa 550
aaagagaagt gtggaaggg aaaatggtct gtgtggaggg gtcaaggagt 600
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactatth ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggatgcttc 800
attccagcct cagggaagcc tggcaccac tgccaacgt gagccagagg 850
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950
gctaccta atgtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtgggtggc cacacctgta attctagcac tttgggaggc 1050
caagggtggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150

gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtagacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base
 <400> 347

cacagttccc caccatcact cntccattc cttccaactt tatttttagc 50
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
 ggagagggac agaggccaga ggactttctca tactggacag aaaccgatca 150
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttcct 200
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
 gggggtggac agcgatggat gctgggtggc gcccctggg atgggccttc 350
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggccca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
 tggatgatgg 509

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 agggacagag gccagaggac ttc 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 caggtgcata ttcacagcag gatg 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 ggaactcccc ttctgcactc acctgttctt gcccctggtg ttcct 45

<210> 351
 <211> 2056
 <212> DNA

[illegible]

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catctgggtt	tgggcagaaa	ggaggggtgct	tcgagagccg	ccctttctga	100
gcttcctggg	cgggctctag	aacaattcag	gcttcgctgc	gactcagacc	150
tcagctccaa	catatgcatt	ctgaagaaag	atggctgaga	tggacagaat	200
gctttatttt	ggaaagaaac	aatgttctag	gtcaaactga	gtctaccaa	250
tgcagacttt	cacaatgggt	ctagaagaaa	tctggacaag	tcttttcatg	300
tggtttttct	acgcattgat	tccatgtttg	ctcacagatg	aagtggccat	350
tctgcctgcc	cctcagaacc	tctctgtact	ctcaaccaac	atgaagcatc	400
tcttgatgtg	gagcccagtg	atcgcgcttg	gagaaacagt	gtactattct	450
gtcgaatacc	agggggagta	cgagagcctg	tacacgagcc	acatctggat	500
ccccagcagc	tggtgctcac	tcaactgaagg	tccctgagtgt	gatgtcactg	550
atgacatcac	ggccactgtg	ccatacaacc	ttcgtgtcag	ggccacattg	600
ggctcacaga	cctcagcctg	gagcatcctg	aagcatccct	ttaatagaaa	650
ctcaaccatc	cttacccgac	ctgggatgga	gatcaccaa	gatggcttcc	700
acctggttat	tgagctggag	gacctggggc	cccagtttga	gttccttgtg	750
gcctactgga	ggagggagcc	tggtgccgag	gaacatgtca	aaatggtgag	800
gagtgggggt	attccagtgc	acctagaaac	catggagcca	ggggctgcat	850
actgtgtgaa	ggcccagaca	ttcgtgaagg	ccattgggag	gtacagcgcc	900
ttcagccaga	cagaatgtgt	ggaggtgcaa	ggagaggcca	ttcccctggt	950
actggccctg	tttgcccttg	ttggcttcat	gctgatacct	gtggctgtgc	1000
cactgttcgt	ctggaaaatg	ggccggctgc	tccagtactc	ctgttgcccc	1050
gtggtggtcc	tcccagacac	cttgaaaata	accaattcac	cccagaagtt	1100
aatcagctgc	agaaggagg	aggtggatgc	ctgtgccacg	gctgtgatgt	1150
ctcctgagga	actcctcagg	gcctggatct	cataggtttg	cggaagggcc	1200
caggtgaagc	cgagaacctg	gtctgcatga	catggaaacc	atgaggggac	1250
aagttgtgtt	tctgttttcc	gccacggaca	agggatgaga	gaagtaggaa	1300
gagcctgttg	tctacaagtc	tagaagoaac	catcagaggc	agggtggttt	1350
gtctaacaga	acactgactg	aggcttaggg	gatgtgacct	ctagactggg	1400

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	125	130	135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	140	145	150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	155	160	165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	170	175	180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	185	190	195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	200	205	210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	215	220	225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					305	310	

<210> 353

<211> 864

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 654, 711, 748, 827

<223> unknown base

<400> 353

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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150

agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtgggt tttctacga ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctgggt ctcaactcact gaaggtcctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
 agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
 ggcgctgggt tgat 864

<210> 354

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 354

aggcttcgct gcgactagac etc 23

<210> 355

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 355

ccaggtcggg taaggatggt tgag 24

<210> 356

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgcac agatgaagtg gccattctgc 50

<210> 357

<211> 1670

<212> DNA

<213> Homo sapiens

<400> 357

cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
tgagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500
ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550
gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
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ataatctcca gggaaacttc gtgccagggc ctcctttctg gggcctggtg 750
aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gcccctgga 800
tgtggagctg aagaggggtc tttatgacct ctttctgccc ccattaaggc 850
tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900
catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950
tcccctcctt tacagccacc gactcagtga actgcggctg ctgtttggag 1000
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gctgaggtgc agctcattca cttcaaccag gaactctacg ggaatttcag 1100
cgctgcctcc cgcggcccca atggcctggc cattctcagc ctctttgtca 1150
acgttgccag tacctctaac ccattcctca gtcgcctcct taaccogagc 1200
accatcactc gcatctccta caagaatgat gcctactttc ttcaagacct 1250

gagcctggag ctctgttcc ctgaatcctt cggcttcac acctatcagg 1300
 gctctctcag caccgccccc tgctccgaga ctgtcacctg gatcctcatt 1350
 gaccggggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400
 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450
 ggcccctgca gcccttggcc cacagggcac tgaggggcaa cagggacccc 1500
 cggcaccccg agaggcgctg ccgaggcccc aactaccgcc tgcattgtga 1550
 tgggtgtccc catggtcgct gagactcccc ttcgaggatt gcacccgccc 1600
 gtctaagcc tccccacaag gcgaggggag ttaccctaa aacaaagcta 1650
 ttaaaggac agaatactta 1670

<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu	1	5	10	15
Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp	20	25	30	
Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe	35	40	45	
Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser	50	55	60	
Leu	Cys	Ala	Val	Gly	Lys	Arg	Gln	Ser	Pro	Val	Asp	Val	Glu	Leu	65	70	75	
Lys	Arg	Val	Leu	Tyr	Asp	Pro	Phe	Leu	Pro	Pro	Leu	Arg	Leu	Ser	80	85	90	
Thr	Gly	Gly	Glu	Lys	Leu	Arg	Gly	Thr	Leu	Tyr	Asn	Thr	Gly	Arg	95	100	105	
His	Val	Ser	Phe	Leu	Pro	Ala	Pro	Arg	Pro	Val	Val	Asn	Val	Ser	110	115	120	
Gly	Gly	Pro	Leu	Leu	Tyr	Ser	His	Arg	Leu	Ser	Glu	Leu	Arg	Leu	125	130	135	
Leu	Phe	Gly	Ala	Arg	Asp	Gly	Ala	Gly	Ser	Glu	His	Gln	Ile	Asn	140	145	150	
His	Gln	Gly	Phe	Ser	Ala	Glu	Val	Gln	Leu	Ile	His	Phe	Asn	Gln	155	160	165	
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<220>
<223> Synthetic oligonucleotide probe

<400> 361
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<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200
gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250
ctgcagtcag caccacgctc gcccccgac gctcgggtgt caggcccttc 300
gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350
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atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500
aaccacagtg ctgttcattg ctagagcaat tccagccatg gtggttccca 550
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gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650
catgcagagt attttgacc ttcataataa attacgaagt cagggtgtatc 700
caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750
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aaattctgat	attgcacttc	ttattttata	taaaataatc	ctttaatatc	2550
caaatgaatc	tgttaaaatg	tttgattcct	tgggaatggc	cttaaaaaata	2600

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 agtaaatgta gggttaagca tggacagcca gagctttcta tgtactgtta 2700
 aaattgaggt cacatatattt cttttgtatc ctggcaaata ctccctgcagg 2750
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 363

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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25						30
Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu
				35				40						45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn
				50				55						60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln
				65				70						75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val
				80				85						90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp
				95				100						105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu
				110				115						120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln
				125				130						135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His
				140				145						150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys
				155				160						165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly

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Cys Ala Ile Asn	Leu Cys His Asn Met	Asn Ile Trp Gly Gln Ile			
	185		190		195
Trp Pro Lys Ala	Val Tyr Leu Val Cys	Asn Tyr Ser Pro Lys Gly			
	200		205		210
Asn Trp Trp Gly	His Ala Pro Tyr Lys	His Gly Arg Pro Cys Ser			
	215		220		225
Ala Cys Pro Pro	Ser Phe Gly Gly Gly	Cys Arg Glu Asn Leu Cys			
	230		235		240
Tyr Lys Glu Gly	Ser Asp Arg Tyr Tyr	Pro Pro Arg Glu Glu Glu			
	245		250		255
Thr Asn Glu Ile	Glu Arg Gln Gln Ser	Gln Val His Asp Thr His			
	260		265		270
Val Arg Thr Arg	Ser Asp Asp Ser Ser	Arg Asn Glu Val Ile Ser			
	275		280		285
Ala Gln Gln Met	Ser Gln Ile Val Ser	Cys Glu Val Arg Leu Arg			
	290		295		300
Asp Gln Cys Lys	Gly Thr Thr Cys Asn	Arg Tyr Glu Cys Pro Ala			
	305		310		315
Gly Cys Leu Asp	Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr			
	320		325		330
Glu Met Gln Ser	Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile			
	335		340		345
Ile Asp Asn Asp	Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg			
	350		355		360
Lys His Tyr Phe	Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile			
	365		370		375
Gly Lys Tyr Gln	Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr			
	380		385		390
Val Gln Ala Val	Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro			
	395		400		405
Phe His Lys Pro	Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg			
	410		415		420
Asn Cys Met Gln	Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr			
	425		430		435
Arg Val Tyr Ser	Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His			
	440		445		450
Ala Gly Val Val	Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro			
	455		460		465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg
485 490 495

Val Phe Ala Val Val
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<210> 364
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 364
ggacagaatt tgggagcaca ctgg 24

<210> 365
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA

<213> Homo sapiens

<400> 369
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ggccagegcc ctccccatgt ccctgctccc acgccgcgcc cctccgggtca 200
gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250
accgcgcgtg tggacgggtc caaatgcaag tgctcccgga agggacccaa 300
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350
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cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450
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aggggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550
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 ataaaatata ttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 370
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 20 25 30
 Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys
 35 40 45
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 50 55 60
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
 65 70 75
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
 80 85 90
 Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys
 95 100 105
 Arg Arg Val Tyr Glu Glu
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<210> 371
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

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tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

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 agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050
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<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30

Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45

Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50					55					60	
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro	
				65					70					75	
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val	
				80					85					90	
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu	
				95					100					105	
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val	
				110					115					120	
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro	
				125					130					135	
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr	
				140					145					150	
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser	
				155					160					165	
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu	
				170					175					180	
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly	
				185					190					195	
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly	
				200					205					210	
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu	
				215					220					225	
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly	
				230					235					240	
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly	
				245					250					255	
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser	
				260					265					270	
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu	
				275					280					285	
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile	
				290					295					300	
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met	
				305					310					315	
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln	
				320					325					330	
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile	
				335					340					345	

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350 355 360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365 370 375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380 385 390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395 400 405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410 415 420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425 430 435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440 445 450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455 460 465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470 475 480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485 490 495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500 505 510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515 520 525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530 535 540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545 550 555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560 565 570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575 580 585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590 595 600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605 610 615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620 625 630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	

	635		640		645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp			
	650	655		660	
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu			
	665	670		675	
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile			
	680	685		690	
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His			
	695	700		705	
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp			
	710	715		720	
Ile Ala His Ile	Gln Asn Glu Glu Ile	Met Ser Leu Gln Met Lys			
	725	730		735	
Gln Leu Glu His	Asp His Glu Cys Glu	Ser Leu Gln Ala His Asp			
	740	745		750	
Thr Leu Arg Leu	Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu Arg			
	755	760		765	
Arg Ser Pro Asp	Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile Thr			
	770	775		780	
Met Ile Pro Asn	Thr Leu Thr Gly Met	Gln Pro Leu His Thr Phe			
	785	790		795	
Asn Thr Phe Ser	Gly Gly Gln Asn Ser	Thr Asn Leu Pro His Gly			
	800	805		810	
His Ser Thr Thr	Arg Val				
	815				

<210> 376
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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 ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100
 ttgttggggg ctgggcaggg gccacagcaa gtcggggcgg gtcaaactgt 150
 cgagtacttg aaacgggagc actcgtctgc gaagccctac caggggtgtg 200
 gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250
 acccagtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300
 gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg caggtgcact 350
 tcaaaatcca tggacaagga aagaagaatc tgcattggga tggcttggca 400
 atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaacat 450
 ggacaaatth gtggggctgg gaggatthgt agacacctac cccaatgagg 500
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 ctagcagctg gttggggact atattctgtc actggagttt tgaatgcagg 1200
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ggccgcatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20					25					30

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly
				35					40					45

Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro
				50					55					60

Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met
				65					70					75

Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp
				80					85					90

Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe
				95					100					105

Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln
				110					115					120

Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr
				125					130					135

Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys
				140					145					150

Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu
				155					160					165

Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn
				170					175					180

Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr
				185					190					195

Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp
				200					205					210

Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met
				215					220					225

Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val
				230					235					240

Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser
				245					250					255

Ile Thr Gly Asp	Leu Ser Asp Asn His	Asp Val Ile Ser Leu Lys
260	265	270
Leu Phe Glu Leu	Thr Val Glu Arg Thr	Pro Glu Glu Glu Lys Leu
275	280	285
His Arg Asp Val	Phe Leu Pro Ser Val	Asp Asn Met Lys Leu Pro
290	295	300
Glu Met Thr Ala	Pro Leu Pro Pro Leu	Ser Gly Leu Ala Leu Phe
305	310	315
Leu Ile Val Phe	Phe Ser Leu Val Phe	Ser Val Phe Ala Ile Val
320	325	330
Ile Gly Ile Ile	Leu Tyr Asn Lys Trp	Gln Glu Gln Ser Arg Lys
335	340	345

Arg Phe Tyr

<210> 381
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 381
 ccttggtcg tggcagcagt gg 22

<210> 382
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 382
 cactctccag gctgcatgct cagg 24

<210> 383
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 383
 gtcaaacgtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
 <211> 3150
 <212> DNA
 <213> Homo sapiens

<400> 384

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ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
tggggctctgg ctcaagaattc ctgcagctgg tgaaaatctg ttttctagaa 200
gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250
ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300
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cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400
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Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	
				215					220					225	
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	
				230					235					240	
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
				245					250					255	
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
				260					265					270	
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	
				275					280					285	
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	
				290					295					300	
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
				305					310					315	
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	
				320					325					330	
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
				335					340					345	
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	
				350					355					360	
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
				365					370					375	
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
				380					385					390	
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
				395					400					405	
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
				410					415					420	
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
				425					430					435	
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
				440					445					450	
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
				455					460					465	
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	
				470					475					480	

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

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 gaggataaag tgaaaatata tggagtagaa gtagaagtaa gggacattaa 750
 cgacaatgcg ctttactttc gtgaaagtga attagaaata aaaattagtg 800
 aaaatgcagc cactgagatg cggttccctc taccaccacgc ctgggatccg 850
 gatatcggga agaactctct gcagagctac gagctcagcc cgaacactca 900
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 tggacagaga ctccggccag aacgcctggc tgtcctaccg tctgctcaag 2200
 gccagcgagc cgggactctt ctcggtgggt ctgcacacgg gcgaggtgcg 2250
 cacggcgcgga gccctgctgg acagagacgc gctcaagcag agcctcgtag 2300
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 cctcgagtct ccagctaact ctgaaacctc agacctcact ctgtacctgg 2450
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 ctgctggcgc tcaggctgcg gcgctggcac aagtcacgcc tgcctgcaggc 2550
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 gggagtttga gaccagcctg accaaccatg agaaaccccg tctatactaa 3150
 aaaaatacaa aattagccgg gcgtggtggt gcatgtctgt aatcccagct 3200
 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggaggtt 3250
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 aaactctatc tca 3313

- <210> 390
- <211> 916
- <212> PRT
- <213> Homo sapiens
- <400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

				290					295					300
Ile	Ser	Thr	Ile	Gly 305	Glu	Leu	Asp	His	Glu 310	Glu	Ser	Gly	Phe	Tyr 315
Gln	Met	Glu	Val	Gln 320	Ala	Met	Asp	Asn	Ala 325	Gly	Tyr	Ser	Ala	Arg 330
Ala	Lys	Val	Leu	Ile 335	Thr	Val	Leu	Asp	Val 340	Asn	Asp	Asn	Ala	Pro 345
Glu	Val	Val	Leu	Thr 350	Ser	Leu	Ala	Ser	Ser 355	Val	Pro	Glu	Asn	Ser 360
Pro	Arg	Gly	Thr	Leu 365	Ile	Ala	Leu	Leu	Asn 370	Val	Asn	Asp	Gln	Asp 375
Ser	Glu	Glu	Asn	Gly 380	Gln	Val	Ile	Cys	Phe 385	Ile	Gln	Gly	Asn	Leu 390
Pro	Phe	Lys	Leu	Glu 395	Lys	Ser	Tyr	Gly	Asn 400	Tyr	Tyr	Ser	Leu	Val 405
Thr	Asp	Ile	Val	Leu 410	Asp	Arg	Glu	Gln	Val 415	Pro	Ser	Tyr	Asn	Ile 420
Thr	Val	Thr	Ala	Thr 425	Asp	Arg	Gly	Thr	Pro 430	Pro	Leu	Ser	Thr	Glu 435
Thr	His	Ile	Ser	Leu 440	Asn	Val	Ala	Asp	Thr 445	Asn	Asp	Asn	Pro	Pro 450
Val	Phe	Pro	Gln	Ala 455	Ser	Tyr	Ser	Ala	Tyr 460	Ile	Pro	Glu	Asn	Asn 465
Pro	Arg	Gly	Val	Ser 470	Leu	Val	Ser	Val	Thr 475	Ala	His	Asp	Pro	Asp 480
Cys	Glu	Glu	Asn	Ala 485	Gln	Ile	Thr	Tyr	Ser 490	Leu	Ala	Glu	Asn	Thr 495
Ile	Gln	Gly	Ala	Ser 500	Leu	Ser	Ser	Tyr	Val 505	Ser	Ile	Asn	Ser	Asp 510
Thr	Gly	Val	Leu	Tyr 515	Ala	Leu	Ser	Ser	Phe 520	Asp	Tyr	Glu	Gln	Phe 525
Arg	Asp	Leu	Gln	Val 530	Lys	Val	Met	Ala	Arg 535	Asp	Asn	Gly	His	Pro 540
Pro	Leu	Ser	Ser	Asn 545	Val	Ser	Leu	Ser	Leu 550	Phe	Val	Leu	Asp	Gln 555
Asn	Asp	Asn	Ala	Pro 560	Glu	Ile	Leu	Tyr	Pro 565	Ala	Leu	Pro	Thr	Asp 570
Gly	Ser	Thr	Gly	Val 575	Glu	Leu	Ala	Pro	Arg 580	Ser	Ala	Glu	Pro	Gly 585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln
				590					595					600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly
				605					610					615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg
				620					625					630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala
				635					640					645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu
				650					655					660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu
				665					670					675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr
				680					685					690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu
				695					700					705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His
				710					715					720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala
				725					730					735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu
				740					745					750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys
				755					760					765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val
				770					775					780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly
				785					790					795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser
				800					805					810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser
				815					820					825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln
				830					835					840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn
				845					850					855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu

	875		880		885
Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp					
	890		895		900
Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro					
	905		910		915

Ala

<210> 391
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 391
 tccgtctctg tgaaccgccc cac 23

<210> 392
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 392
 ctcgggcgca ttgtcgttct ggtc 24

<210> 393
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 393
 ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394
 <211> 999
 <212> DNA
 <213> Homo sapiens

<400> 394
 cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50
 cccagttaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100
 ggggcctcct ccaactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
 aggaggacaa ggtgctgggg ggtcatgagt gccaaaccca ttgcgcagcct 300
 tggcaggcgg ccttggtcca gggccagcaa ctactctgtg gcggtgtcct 350
 tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400
 acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450
 caagaaatac ctgtggttca gtccatccca caccctgtct acaacagcag 500
 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
 aggcattcct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600
 acccagcctg gccagaagtg caccgtctca ggctggggca ctgtcaccag 650
 tccccgagag aattttcctg acactctcaa ctgtgcagaa gtaaaaatct 700
 ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750
 atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800
 tggaggcccc ctggtgtgtg atggtgcact ccagggcac acatcctggg 850
 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900
 tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950
 ctaggataag cactagatct cccttaataa actcacaact ctctgggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
				245					250					255
Ile	Gly	Ser	Lys	Gly										
				260										

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccggccc gccgcgccgc ccacgcccc accccggccc gcgcccccta 100
gccccgccc gggcccgcg ccgcgccgc gccaggtga gcgctccgcc 150
cgccgcgagg ccccgcccc gccgccccc gccccgccc ggccggcggg 200
ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250
tcatectccc ggggggccgc gctgcgagcg ccccgccagt ccgcgccgcc 300
gccgccctcg ccctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccag 350
cccagccaga gccggggcga gcggagcgcg ccgagcctcg tcccgcggcc 400
gggcccgggc cgggccgtag cggcgcgcc tggatgcgga cccggccgcg 450
gggagacggg cggccgcccc gaaacgactt tcagtccccg acgcgccccg 500
cccaaccct acgatgaaga gggcgctccgc tggaggagc cggctgctgg 550
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gcctgcgtat gctacaatga gcccaaggcg acgacaagct gccccagca 650
gggcctgcag gctgtgccc tgggcatccc tgctgccagc cagcgcatct 700
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tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800
tgatgaggct gccttactg gcctggccct cctggagcag ctggacctca 850
gcgataatgc acagctccgg tctgtggacc ctgccacatt ccacggcctg 900
ggccgcctac acacgtgca cctggaccgc tcgggcctgc aggagctggg 950
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acaacgcgct gcaggcactg cctgatgaca ccttccgca cctgggcaac 1050
ctcacacacc tcttcctgca cggcaaccgc atctccagcg tgcccagagc 1100

cgcccttcggt gggtgcaca gcctcgaccg tctcctactg caccagaacc 1150
 gcggtggccca tgtgcacccg catgccttcc gtgaccttgg ccgcctcatg 1200
 aactctatc tgtttgccaa caatctatca gcgctgcca ctgaggccct 1250
 ggccccctg cgtgccctgc agtacctgag gctcaacgac aaccctggtg 1300
 tgtgtgactg ccgggcacgc ccactctggg cctgggtgca gaagttccgc 1350
 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400
 tgacctcaaa cgcctagctg ccaatgacct gcagggctgc gctgtggcca 1450
 ccggccctta ccatcccatc tggaccggca gggccaccga tgaggagccg 1500
 ctggggcttc ccaagtgtg ccagccagat gccgctgaca aggcctcagt 1550
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 tgccgcccgg tgacagcccg ccgggcaacg gctctggccc acggcacatc 1650
 aatgactcac cctttgggac tctgcctggc tctgctgagc cccgctcac 1700
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 ctgcgccgag gccaggctgt tcacgcaaga accgcaccgg cagccactgc 1800
 cgtctggggc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850
 ctcaagtgcc ctaccagcc tcacctgag cctcaccccc ctgggcctgg 1900
 cgctggtgct gtggacagtg cttggggcct gctgaccccc agcggacaca 1950
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000
 ccgccaagcc agccgggcgg ccgaccctg gggcaggcca ggccagggtcc 2050
 tccctgatgg acgcctgccg cccgccacc ccatctccac cccatcatgt 2100
 ttacaggggt cggcggcagc gtttgttcca gaacgccgcc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20					25					30	

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

<220>
<223> Synthetic oligonucleotide probe

<400> 403
aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404
<211> 2738
<212> DNA
<213> Homo sapiens

<400> 404
ggaagtcac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50
ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
cgcggcggaa cctagaagct attctgtggt ggaggaaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350
tccaggcggg gggttagggg tgtttccaga ggaacaaac tacatttgca 400
gctcaatcag gagaccgcg atttgttgct aaatgagaaa ttggaccgtg 450
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
ctagagagtc ctttcagatt ttttcaagct gagctgcaag taatagacat 550
aaacgaccac tctccagtat ttctggacaa acaaagtgtg gtgaaagtat 600
cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650
ttagatgtag gccaaaaca tattgagaac tatataatca gcccactc 700
ctattttcgg gtccctcacc gcaaacgcag tgatggcagg aaatacccag 750
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agatcaatcc cttgacagga gaaattgaac taaaaaaca actcgatttc 1100
gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

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atgccccaga agttaccatg tctgcattta ccagcccaat acctgagaac 1250
gcgccctgaaa ctgtggttgc acttttccagt gtttcagatc ttgattcagg 1300
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attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650
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tgttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405
<211> 798
<212> PRT
<213> Homo sapiens

<400> 405
Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu
1 5 10 15
Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu
20 25 30
Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
35 40 45
Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
50 55 60
Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
65 70 75
Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
80 85 90
Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
95 100 105
Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
110 115 120
Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
125 130 135
Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
140 145 150
Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln
155 160 165
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg
170 175 180
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu
185 190 195
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg
200 205 210
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly
215 220 225
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	435
Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala	440	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser	455	465
Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser	470	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp	485	495
Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn	500	510
Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln	515	525

Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	
				530					535					540	
Leu	Ser	Ser	Glu	Ala	Leu	Val	Arg	Val	Val	Val	Leu	Asp	Ala	Asn	
				545					550					555	
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	
				560					565					570	
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
				575					580					585	
Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
				590					595					600	
Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
				605					610					615	
Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	
				620					625					630	
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
				635					640					645	
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	
				650					655					660	
Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	
				665					670					675	
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	
				680					685					690	
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
				695					700					705	
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
				755					760					765	
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
				770					775					780	
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
				785					790					795	
Asn	Ile	Gln													

<210> 406

<211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 406
 ctgagaacgc gcctgaaact gtg 23

 <210> 407
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 407
 agcgttgtca ttgacatcgg cg 22

 <210> 408
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 408
 ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

 <210> 409
 <211> 1379
 <212> DNA
 <213> Homo sapiens

 <400> 409
 acccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50
 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
 cggctcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
 agtggtcgct tatggtcaga ggagcagcct gtcaccctc tccagggtggg 250
 ggctgtgtac ctgggtgagg aggagctcct gcatgacccg atggggccagg 300
 acagggcagc agaagaggcc aatgcggtgc tggggctgga caccgaaggc 350
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500

cacttcctg acagagaaga ggagtattac acagagccag aagtggcgga 550
atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600
ccccaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
actctgaaaa ttttaaatat gtcacaggac cttatggatt ttctgaaccc 700
aaacggtagt gactgtactc tagtcctgtt ttacaccccg tggtgccgct 750
tttctgccag tttggcccct cactttaact ctctgccccg ggcattttcca 800
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cagggtttggc accgtagctg ttcctaataat tttattatit caaggagcta 900
aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950
atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000
aactcaagcc gaccaaatag gccctcttcc cagcactttg ataaaaagtg 1050
tggaactggtt gcttgtatit tccttattct ttttaattag ttttattatg 1100
tatgctacca ttcgaactga gagtattcgg tggctaattc caggacaaga 1150
gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200
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agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300
aacaactgaa tgtataaaaa aattataaac tgggtgtttta actagtattg 1350
caataagcaa atgcaaaaat attcaatag 1379

<210> 410

<211> 360

<212> PRT

<213> Homo sapiens

<400> 410

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Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val
				20					25					30

Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45

Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60

Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75

Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80										85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val					
				95					100					105					
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu					
				110					115					120					
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly					
				125					130					135					
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu					
				140					145					150					
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn					
				155					160					165					
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg					
				170					175					180					
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met					
				185					190					195					
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys					
				200					205					210					
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser					
				215					220					225					
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu					
				230					235					240					
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr					
				245					250					255					
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly					
				260					265					270					
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
				350					355					360					

<210> 411
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
cacagagcca gaagtggcgg aatc 24

<210> 412
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccacatgttc ctgctcttgc cctgg 25

<210> 413
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cggtagtgc tgtactctag tcctgtttta caccctgtgg tgccg 45

<210> 414
<211> 1196
<212> DNA
<213> Homo sapiens

<400> 414
cccggctccg ctccctctgc ccctcgggg tcgcgcgccc acgatgctgc 50
agggccctgg ctgctgctg ctgctcttcc tcgcctcgca ctgctgcctg 100
ggctcggcgc gcgggctctt cctctttggc cagcccgcact tctcctacaa 150
gcgcagcaat tgcaagccca tcccgggtcaa cctgcagctg tgccacggca 200
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gcccgcacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500
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agcttcccc tgcttttgc acgtttgcat cccagcatt tcctgagtta 1100
taaggccaca ggagtggata gctgttttca cctaaaggaa aagccacccc 1150
gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met	Leu	Gln	Gly	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser	1	5	10	15
His	Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln	20	25	30	
Pro	Asp	Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val	35	40	45	
Asn	Leu	Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu	50	55	60	
Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln	65	70	75	
Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp	80	85	90	
Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp	95	100	105	
Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln	110	115	120	
Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly	Phe	Pro	125	130	135	

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
 cctggctcgc tgctgctgct c 21

<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150
gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
tcctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250
tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300
ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350
tacgcatggg gccctgcatg gttgttggga cccaaaaccc atttgccctc 400
ctcatgggtg gccagagcct ctgtgccctt gccagagacc tggatcatctt 450
ctctccagcc aagctggctg ccttgtggtt ccagagcac cagcagacca 500
cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550
aatgtgctgt ccctgtgtct ggtcaagaag ggtgaggaca ttccgttaat 600
gctcgggtgc tataccatcc ctgctggcgt cgtctgcctg ctgtccacca 650
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<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

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Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
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Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val

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Gly Thr Gln Asn	Pro Phe Ala Phe Leu	Met Gly Gly Gln Ser	Leu		
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Cys Ala Leu Ala	Gln Ser Leu Val Ile	Phe Ser Pro Ala Lys	Leu		
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Ala Ala Leu Trp	Phe Pro Glu His Gln	Arg Ala Thr Ala Asn	Met		
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Leu Ala Thr Met	Ser Asn Pro Leu Gly	Val Leu Val Ala Asn	Val		
	170	175		180	
Leu Ser Pro Val	Leu Val Lys Lys Gly	Glu Asp Ile Pro Leu	Met		
	185	190		195	
Leu Gly Val Tyr	Thr Ile Pro Ala Gly	Val Val Cys Leu Leu	Ser		
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Thr Ile Cys Leu	Trp Glu Ser Val Pro	Pro Thr Pro Pro Ser	Ala		
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Gly Ala Ala Ser	Ser Thr Ser Glu Lys	Phe Leu Asp Gly Leu	Lys		
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Leu Gln Leu Met	Trp Asn Lys Ala Tyr	Val Ile Leu Ala Val	Cys		
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Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu	Leu		
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Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly		
	275	280		285	
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Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala		
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Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe		
	320	325		330	
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala		
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Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val		
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Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly		
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Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile		
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Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu		
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Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala
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Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg
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Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr
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Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala
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Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
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Pro Trp Val Ile Thr
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<213> Artificial Sequence

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<400> 421
agcttctcag ccctcctgga gcag 24

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cggttcaata aacctggacg cttgg 25

<210> 423
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<223> Synthetic oligonucleotide probe

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tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

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				20					25					30	
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	
				35					40					45	
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	
				50					55					60	
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	
				65					70					75	
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	
				80					85					90	
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	
				95					100					105	
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	
				110					115					120	
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	
				125					130					135	
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	
				140					145					150	
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	
				155					160					165	
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	
				170					175					180	
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	
				185					190					195	

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Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr			
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Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser			
	530		535		540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu			
	545		550		555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu			
	560		565		570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr			
	575		580		585
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro			
	590		595		600
Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro			
	605		610		615
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala			
	620		625		630
Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His			
	635		640		645
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val			
	650		655		660
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile			
	665		670		675
Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu			
	680		685		690
Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser			
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Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile			
	710		715		720
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu			
	725		730		735
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr			
	740		745		750
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg			
	755		760		765
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val			
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Leu	Arg	Gly	Gln	Ala	Gly	Glu	Pro	Cys	Glu	Val	Gly	Gln	Ser	His		
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Lys	Asp	Val	Asp	Lys	Glu	Ala	Met	Met	Glu	Ala	Gly	Trp	Asp	Pro		
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Cys	Leu	Gln	Ala	Pro	Phe	His	Leu	Thr	Pro	Thr	Leu	Tyr	Arg	Thr		
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Leu	Arg	Asn	Gln	Gly	Asn	Gln	Gly	Ala	Pro	Ala	Glu	Ser	Arg	Glu		
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Val	Leu	Gln	Asp	Thr	Val	Asn	Leu	Leu	Phe	Asn	His	Pro	Arg	Gln		
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Arg	Asn	Ala	Ser	Arg	Glu	Asn	Leu	Asn	Leu	Pro	Glu	Pro	Gln	Pro		
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Pro	Lys	Pro	Asn	His	Arg	Gly	Asn	Lys	Tyr	Leu	Ala	Lys	Pro	Gly		
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Gly	Ser	Arg	Ser	Ala	Ile	Pro	Asp	Thr	Asp	Gly	Pro	Ser	Ala	Arg		
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Pro	Glu	Glu	Asp	Leu	Ser	Val	Lys	Gln	Leu	Leu	Glu	Glu	Glu	Leu		
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Ser	Ser	Leu	Leu	Asp	Pro	Ser	Thr	Gly	Leu	Ala	Leu	Asp	Arg	Leu		
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Ser	Ala	Pro	Asp	Pro	Ala	Trp	Met	Ala	Arg	Leu	Ser	Leu	Pro	Leu		
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<212> DNA
<213> Homo sapiens

<400> 429

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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
				35					40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
				50					55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
				65					70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
				80					85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
				95					100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
				110					115					120

Met	Tyr	Phe	Phe	Trp 125	Lys	Leu	Gly	Asp	Pro 130	Phe	Pro	Ile	Leu	Ser 135
Pro	Lys	His	Gly	Ile 140	Leu	Ser	Ile	Glu	Gln 145	Leu	Ile	Ser	Arg	Val 150
Gly	Val	Ile	Gly	Val 155	Thr	Leu	Met	Ala	Leu 160	Leu	Ser	Gly	Phe	Gly 165
Ala	Val	Asn	Cys	Pro 170	Tyr	Thr	Tyr	Met	Ser 175	Tyr	Phe	Leu	Arg	Asn 180
Val	Thr	Asp	Thr	Asp 185	Ile	Leu	Ala	Leu	Glu 190	Arg	Arg	Leu	Leu	Gln 195
Thr	Met	Asp	Met	Ile 200	Ile	Ser	Lys	Lys	Lys 205	Arg	Met	Ala	Met	Ala 210
Arg	Arg	Thr	Met	Phe 215	Gln	Lys	Gly	Glu	Val 220	His	Asn	Lys	Pro	Ser 225
Gly	Phe	Trp	Gly	Met 230	Ile	Lys	Ser	Val	Thr 235	Thr	Ser	Ala	Ser	Gly 240
Ser	Glu	Asn	Leu	Thr 245	Leu	Ile	Gln	Gln	Glu 250	Val	Asp	Ala	Leu	Glu 255
Glu	Leu	Ser	Arg	Gln 260	Leu	Phe	Leu	Glu	Thr 265	Ala	Asp	Leu	Tyr	Ala 270
Thr	Lys	Glu	Arg	Ile 275	Glu	Tyr	Ser	Lys	Thr 280	Phe	Lys	Gly	Lys	Tyr 285
Phe	Asn	Phe	Leu	Gly 290	Tyr	Phe	Phe	Ser	Ile 295	Tyr	Cys	Val	Trp	Lys 300
Ile	Phe	Met	Ala	Thr 305	Ile	Asn	Ile	Val	Phe 310	Asp	Arg	Val	Gly	Lys 315
Thr	Asp	Pro	Val	Thr 320	Arg	Gly	Ile	Glu	Ile 325	Thr	Val	Asn	Tyr	Leu 330
Gly	Ile	Gln	Phe	Asp 335	Val	Lys	Phe	Trp	Ser 340	Gln	His	Ile	Ser	Phe 345
Ile	Leu	Val	Gly	Ile 350	Ile	Ile	Val	Thr	Ser 355	Ile	Arg	Gly	Leu	Leu 360
Ile	Thr	Leu	Thr	Lys 365	Phe	Phe	Tyr	Ala	Ile 370	Ser	Ser	Ser	Lys	Ser 375
Ser	Asn	Val	Ile	Val 380	Leu	Leu	Leu	Ala	Gln 385	Ile	Met	Gly	Met	Tyr 390
Phe	Val	Ser	Ser	Val 395	Leu	Leu	Ile	Arg	Met 400	Ser	Met	Pro	Leu	Glu 405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu		
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440	445	450
Lys Gln Met Ala Pro		
455		

<210> 431
 <211> 407
 <212> DNA
 <213> Homo sapiens

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 <222> 78, 81, 113, 157, 224, 297
 <223> unknown base

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 <210> 432
 <211> 457
 <212> DNA
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 <220>
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 <222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
 <223> unknown base

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a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45
Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60
Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly

80										85					90				
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg					
				95					100					105					
Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
				110					115					120					
Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
				125					130					135					
Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
				140					145					150					
Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
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Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
				170					175					180					
Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
				185					190					195					
Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
				200					205					210					
Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
				215					220					225					
Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
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Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
				245					250					255					
Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
				260					265					270					
Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
				275					280					285					
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
				290					295					300					
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
				305					310					315					
Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
				335					340					345					
Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
				350					355					360					
Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
				365					370					375					

Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala	
				380					385					390	
Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	
				395					400					405	
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	
				410					415					420	
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	
				425					430					435	
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	
				440					445					450	
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	
				455					460					465	
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	
				470					475					480	
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	
				485					490					495	
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	
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Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr	
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Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu	
				545					550					555	
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln	
				560					565					570	
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn	
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Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser	
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Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
				605					610					615	
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln	
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Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	
				635					640					645	
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr	
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Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp	

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				680						685					690				
Leu	Glu	Leu	Met	Val	Thr	Asn	Leu	Pro	Ser	Asp	Pro	Ala	Gln	Pro					
				695					700					705					
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu		Ala	Gln	Leu	Leu	Val	Met				
				710					715					720					
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro					
				725					730					735					
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val					
				740					745					750					
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr					
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Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr					
				770					775					780					
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu					
				785					790					795					
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro					
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Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser					
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Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val					
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Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro					
				860					865					870					
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val					
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Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser					
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Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg					
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Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn					
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Cys	Val	Val	Phe	Ser	Cys	Pro	Leu	Tyr	Ser	Phe	Asp	Arg	Ala	Ala	
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Val	Leu	His	Val	Trp	Gly	Arg	Leu	Trp	Asn	Ser	Thr	Phe	Leu	Glu	
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Glu	Tyr	Ser	Ala	Val	Lys	Ser	Leu	Glu	Val	Ile	Val	Arg	Ala	Asn	
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Ile	Thr	Val	Lys	Ser	Ser	Ile	Lys	Asn	Leu	Met	Leu	Arg	Asp	Ala	
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				1040					1045					1050	
Ala	Gly	Leu	Leu	Val	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Trp	Lys	
				1055					1060					1065	
Met	Gly	Phe	Phe	Lys	Arg	Ala	Lys	His	Pro	Glu	Ala	Thr	Val	Pro	
				1070					1075					1080	
Gln	Tyr	His	Ala	Val	Lys	Ile	Pro	Arg	Glu	Asp	Arg	Gln	Gln	Phe	
				1085					1090					1095	
Lys	Glu	Glu	Lys	Thr	Gly	Thr	Ile	Leu	Arg	Asn	Asn	Trp	Gly	Ser	
				1100					1105					1110	
Pro	Arg	Arg	Glu	Gly	Pro	Asp	Ala	His	Pro	Ile	Leu	Ala	Ala	Asp	
				1115					1120					1125	
Gly	His	Pro	Glu	Leu	Gly	Pro	Asp	Gly	His	Pro	Gly	Pro	Gly	Thr	
				1130					1135					1140	

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgcctct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcca gcacagtgtc ggctcacaac aagatgtctc aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttgggtg cagtcagtct ctgcagctg 200
ccgcggcggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250
gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
ggagtccagg aaaacccttc gatcaggcctt tagatccagc taaggatcca 400
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aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtotta 1850
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ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
aaaaaaaaaa aaaa 1964

<210> 442
<211> 436
<212> PRT
<213> Homo sapiens

<400> 442
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Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly
20 25 30
Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu
35 40 45
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

				50						55					60
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro	
				65					70					75	
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys	
				80					85					90	
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp	
				95					100					105	
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg	
				110					115					120	
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile	
				125					130					135	
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val	
				140					145					150	
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu	
				155					160					165	
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu	
				170					175					180	
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg	
				185					190					195	
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala	
				200					205					210	
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser	
				215					220					225	
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg	
				230					235					240	
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp	
				245					250					255	
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln	
				260					265					270	
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr	
				275					280					285	
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile	
				290					295					300	
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro	
				305					310					315	
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val	
				320					325					330	
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly	
				335					340					345	

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
				425					430					435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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cagggatggg cgacaagatc tggctgccct tccccgtgct ccttctggcc 150
gctctgcctc cggtgctgct gcctggggcg gccggcttca caccttccct 200
cgatagcgac ttcaccttta cccttccgc cgccagaag gagtgtttct 250
accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400
ctgaagttag tgattacatg ttctgctttg acaatacatt cagcaccatt 450
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tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
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ctatggttaa tttagtggtc atggtgggtg tgcagccat tcaagtttat 750
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 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60
Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75
Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90
Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105
Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile

110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu		
125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp		
140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser		
155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe		
170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val		
185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser		
200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg		
215	220	225
Lys Ser Arg Thr		

<210> 448
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 448
 cccagcaggg ctgggcgaca aga 23

<210> 449
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 gtcttcaggt ttcatatcca ata 23

<210> 450
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
 ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451
 <211> 859
 <212> DNA
 <213> Homo sapiens

<400> 451
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 gccctgcca gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150
 tcagggtcaa ggtgaagaaa ccagaaagga actgccctct ccacggatca 200
 gctgtcccaa aggtccaag gcctatggct cccctgcta tgccttggtt 250
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 ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350
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<210> 452
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 452
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 20 25 30
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
 35 40 45
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

					50						55						60	
Trp	Met	Asp	Ala	Asp 65	Leu	Ala	Cys	Gln	Lys 70	Arg	Pro	Ser	Gly	Lys 75				
Leu	Val	Ser	Val	Leu 80	Ser	Gly	Ala	Glu	Gly 85	Ser	Phe	Val	Ser	Ser 90				
Leu	Val	Arg	Ser	Ile 95	Ser	Asn	Ser	Tyr	Ser 100	Tyr	Ile	Trp	Ile	Gly 105				
Leu	His	Asp	Pro	Thr 110	Gln	Gly	Ser	Glu	Pro 115	Asp	Gly	Asp	Gly	Trp 120				
Glu	Trp	Ser	Ser	Thr 125	Asp	Val	Met	Asn	Tyr 130	Phe	Ala	Trp	Glu	Lys 135				
Asn	Pro	Ser	Thr	Ile 140	Leu	Asn	Pro	Gly	His 145	Cys	Gly	Ser	Leu	Ser 150				
Arg	Ser	Thr	Gly	Phe 155	Leu	Lys	Trp	Lys	Asp 160	Tyr	Asn	Cys	Asp	Ala 165				
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<210> 453
<211> 550
<212> DNA
<213> Homo sapiens
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<210> 454
<211> 125
<212> PRT
<213> Homo sapiens
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<400> 454

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20 25 30
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
35 40 45
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
50 55 60
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
65 70 75
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
80 85 90
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
95 100 105
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
110 115 120
Leu Ser Leu Arg Leu
125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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gcgagcgagg agctaccgg gtctttgtcg cgatggtagc ggcggtcttc 200
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 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttta 1050
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 gagtctagaa cgcaaggatc tcttggaatg acaaatagata ggtacctaaa 1400
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
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<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

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				20					25					30
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu
				35					40					45
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val
				50					55					60
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln
				65					70					75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	80	85	90
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	95	100	105
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	110	115	120
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	125	130	135
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	140	145	150
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	155	160	165
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	170	175	180
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	185	190	195
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	200	205	210
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	215	220	225
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	230	235	240
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	245	250	255
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 <223> unknown base

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<212> DNA

<213> Homo sapiens

<400> 458

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 gaaataagac aagctttcaa gaaattggca ttgaagttaac atcctgataa 600
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 ggagaaaagg gacttgagga taatcaagggt ggccagtatg aaagctggaa 750
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75
 Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu
 80 85 90
 Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu
 95 100 105
 Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr
 110 115 120
 Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu
 125 130 135
 Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe
 140 145 150
 Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala
 155 160 165
 Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg
 170 175 180
 Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met
 185 190 195
 Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly

				200					205					210
Met	Ala	Pro	Val	Lys 215	Tyr	His	Gly	Asp	Arg 220	Ser	Lys	Glu	Ser	Leu 225
Val	Ser	Phe	Ala	Met 230	Gln	His	Val	Arg	Ser 235	Thr	Val	Thr	Glu	Leu 240
Trp	Thr	Gly	Asn	Phe 245	Val	Asn	Ser	Ile	Gln 250	Thr	Ala	Phe	Ala	Ala 255
Gly	Ile	Gly	Trp	Leu 260	Ile	Thr	Phe	Cys	Ser 265	Lys	Gly	Gly	Asp	Cys 270
Leu	Thr	Ser	Gln	Thr 275	Arg	Leu	Arg	Leu	Ser 280	Gly	Met	Leu	Phe	Leu 285
Asn	Ser	Leu	Asp	Ala 290	Lys	Glu	Ile	Tyr	Leu 295	Glu	Val	Ile	His	Asn 300
Leu	Pro	Asp	Phe	Glu 305	Leu	Leu	Ser	Ala	Asn 310	Thr	Leu	Glu	Asp	Arg 315
Leu	Ala	His	His	Arg 320	Trp	Leu	Leu	Phe	Phe 325	His	Phe	Gly	Lys	Asn 330
Glu	Asn	Ser	Asn	Asp 335	Pro	Glu	Leu	Lys	Lys 340	Leu	Lys	Thr	Leu	Leu 345
Lys	Asn	Asp	His	Ile 350	Gln	Val	Gly	Arg	Phe 355	Asp	Cys	Ser	Ser	Ala 360
Pro	Asp	Ile	Cys	Ser 365	Asn	Leu	Tyr	Val	Phe 370	Gln	Pro	Ser	Leu	Ala 375
Val	Phe	Lys	Gly	Gln 380	Gly	Thr	Lys	Glu	Tyr 385	Glu	Ile	His	His	Gly 390
Lys	Lys	Ile	Leu	Tyr 395	Asp	Ile	Leu	Ala	Phe 400	Ala	Lys	Glu	Ser	Val 405
Asn	Ser	His	Val	Thr 410	Thr	Leu	Gly	Pro	Gln 415	Asn	Phe	Pro	Ala	Asn 420
Asp	Lys	Glu	Pro	Trp 425	Leu	Val	Asp	Phe	Phe 430	Ala	Pro	Trp	Cys	Pro 435
Pro	Cys	Arg	Ala	Leu 440	Leu	Pro	Glu	Leu	Arg 445	Arg	Ala	Ser	Asn	Leu 450
Leu	Tyr	Gly	Gln	Leu 455	Lys	Phe	Gly	Thr	Leu 460	Asp	Cys	Thr	Val	His 465
Glu	Gly	Leu	Cys	Asn 470	Met	Tyr	Asn	Ile	Gln 475	Ala	Tyr	Pro	Thr	Thr 480
Val	Val	Phe	Asn	Gln 485	Ser	Asn	Ile	His	Glu 490	Tyr	Glu	Gly	His	His 495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro
				500					505					510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr
				515					520					525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro
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Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met
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Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys
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Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr
				575					580					585
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln
				590					595					600
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg
				605					610					615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr
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Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp
				635					640					645
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
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Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
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Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
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Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu			
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 <223> Synthetic oligonucleotide probe

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<210> 461
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 461
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<210> 462
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
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<210> 463
<211> 1818
<212> DNA
<213> Homo sapiens

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caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150
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<212> PRT
<213> Homo sapiens

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His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	
				50					55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	
				65					70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	
				80					85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	
				95					100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	
				110					115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	
				125					130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	
				140					145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	
				155					160					165	
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	
				170					175					180	
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	
				185					190					195	
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	
				200					205					210	
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	
				215					220					225	
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	
				230					235					240	
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	
				245					250					255	
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	
				260					265					270	
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	
				275					280					285	
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	
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<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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gagaggggccc agcccccccc gggcaggatg accaaggccc ggctgttccg 150
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actgggacag cgcaggcgcc ggcacttct acttgcacac gtccttctct 250
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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu
335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp
410

<210> 467
<211> 1071
<212> DNA
<213> Homo sapiens

<400> 467
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gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
tggagcagga gtcacctgga gctgtcttta tcctctgtga tgtgactcag 300
gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350
cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	
				125					130					135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	
				140					145					150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	
				155					160					165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	
				170					175					180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	
				185					190					195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	
				200					205					210	
Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly	
				215					220					225	
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly	
				230					235					240	
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	
				245					250					255	
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser	
				260					265					270	

<210> 469

<211> 687

<212> DNA

<213> Homo sapiens

<400> 469

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ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
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20 25 30
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
140 145 150
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

<400> 471
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ctccccgcgc agaagcctcg ctgggcgccc aacatggcgg gtgggcgctg 150
cggcccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200
cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300
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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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			20						25					30
Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
			35						40					45
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
			50						55					60
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
			65						70					75
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
			80						85					90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr
				170					175					180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala
				185					190					195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile
				200					205					210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg
				215					220					225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln
				230					235					240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu
				245					250					255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu
				260					265					270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu
				275					280					285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly
				290					295					300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu
				305					310					315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr
				320					325					330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala
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Asp Lys Gly Leu

<210> 473
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 473
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<210> 474
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 474
ctctcctcat ccacaccagc agcc 24

<210> 475
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

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agaaattgta ccaattttac taaattatgc agtttaaaat ggatgatttt 2400
atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaaa 2450
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

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Thr	Gln	Leu	His	Phe	Asp	Ser	Gln	Ser	Asn	Thr	Arg	Ile	Ala	Val	20	25	30	
Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
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<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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				20				25						30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35				40						45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50				55						60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65				70						75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
				80					85					90	
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
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Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
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Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
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Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
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Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
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Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
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Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

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Ser Cys Phe Cys	Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val			
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Ser Ser Val Glu	Val Asp Ala Val His	Lys His Tyr Leu Ser Leu			
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Leu Ser Tyr Val	Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val			
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Thr Ile Ala Ala	Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg			
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Arg Lys Pro Arg	Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu			
	440	445			450
Leu Ala Val Phe	Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro			
	455	460			465
Val Ala Leu Thr	Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile			
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Phe Leu His Phe	Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu			
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Glu Gly Tyr Asn	Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr			
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Tyr Val Pro Gly	Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly			
	515	520			525
Phe Pro Ile Phe	Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp			
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Asn Tyr Gly Pro	Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly			
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Val Ile Tyr Pro	Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser			
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Tyr Ile Thr Asn	Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn			
	575	580			585
Met Ala Met Leu	Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg			
	590	595			600
Pro His Thr Gln	Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu			
	605	610			615
Ser Leu Val Leu	Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe			
	620	625			630
Ala Ser Gly Thr	Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile			
	635	640			645
Ile Thr Ser Phe	Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser			
	650	655			660

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Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
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<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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<400> 485
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<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

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<221> unsure
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<223> unknown base

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	
Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180	
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr	185	190	195	

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Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
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Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
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Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
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Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
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Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
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Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
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Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
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<213> Homo sapiens

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<211> 1049

<212> PRT

<213> Homo sapiens

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Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	
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Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	
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Leu	Lys	Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser	
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Thr	Leu	Thr	Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile	
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Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
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Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	935	940	945
Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	950	955	960
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	965	970	975
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	980	985	990
Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	995	1000	1005
Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	1010	1015	1020
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	1025	1030	1035
Asp	Asn	His	Val	Ala	Tyr	Ser	Gln	Val	Phe	Lys	Glu	Thr	Val		1040	1045	

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<211> 4199

<212> DNA

<213> Homo sapiens

<400> 497

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Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro Cys
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275	280	285
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Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val
305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser
335	340	345

Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	
				350					355					360	
Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	
				365					370					375	
Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	
				380					385					390	
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	
				395					400					405	
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	
				410					415					420	
Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	
				425					430					435	
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	
				440					445					450	
Ile	Arg	Lys	Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	
				455					460					465	
Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	
				470					475					480	
Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe	Phe	
				485					490					495	
Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	Asp	Ile	Ala	Cys	Leu	
				500					505					510	
Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu	
				515					520					525	
Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	Thr	Asn	Asn	
				530					535					540	
Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Asp	
				545					550					555	
Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	Ile	
				560					565					570	
Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	
				575					580					585	
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	
				590					595					600	
Asp	Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	
				605					610					615	
Ser	Gly	Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	
				620					625					630	
Tyr	Ile	Ser	Ile	Phe	Lys	Gly	Leu	Lys	Asn	Leu	Thr	Arg	Leu	Asp	

635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	
650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	
665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	
680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	
695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	
710	715	720
His Asn Arg Ile Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	
725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	
740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	
755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	
770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	
785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	
800	805	810
Gly Lys Ser Ile Val Ser Leu Glu Leu	Thr Thr Cys Val Ser Asp	
815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe	Thr Phe Phe Ile Thr Thr	
830	835	840
Met Val Met Leu Ala Ala Leu Ala His	His Leu Phe Tyr Trp Asp	
845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu	Ala Lys Val Lys Gly Tyr	
860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile Ser	
875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr	Asp Trp Val Ile Asn Glu	
890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg	Asp Lys Asn Val Leu Leu	
905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro	Gly Leu Ala Ile Ile Asp	
920	925	930

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 502
gccgagacaa aaacgttctc c 21

<210> 503
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 503
catccatgtt ctcatccatt agcc 24

<210> 504
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 504
tcgacaacct catgcagagc atcaaccaaa gcaagaaaac agtatt 46

<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 505
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ggctgcaagg gaggctcctg tggacaggcc aggcagggtg gcctcaggag 150
gtgcctccag gcggccagtg ggcctgaggc cccagcaagg gctaggggtcc 200
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250
cagcagcatc agcagcccc aggaccgggg aggcacagggt ggccccacc 300
accgggagga gcagctcctg cccctgtccg ggggatgact gattctctc 350
cgccaggcca cccagaggag aaggccaccc cgcctggagg cacaggccat 400
gaggggtctc caggaggtgc tgctgatgtg gcttctggtg ttggcagtgg 450
gcggcacaga gcacgcctac cggcccggcc gtaggggtgtg tgctgtccgg 500

gtcaogggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550
cttctcacc acctgcgacg ggcaccgggc ctgcagcacc taccgaacca 600
tctataggac cgcctaccgc cgcagccctg ggctggcccc tgccaggcct 650
cgctacgcgt gctgccccgg ctggaagagg accagcgggc ttcctggggc 700
ctgtggagca gcaatatgcc agccgccatg ccggaacgga gggagctgtg 750
tccagcctgg ccgctgccgc tgccctgcag gatggcgggg tgacacttgc 800
cagtcagatg tggatgaatg cagtgcctag aggggcggct gtccccagcg 850
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tggccccact gcacagcctg gcctcgcagg cactggagca tgggctcccg 1100
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ctcacgccgc cctgcagccc ccatgccct gcccaacatg ctgggggtcc 1300
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gctgggtggg gcctcagtgg gggctgctgc ctgaccccca gcacaataaa 1600
aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1700
gccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506
<211> 273
<212> PRT
<213> Homo sapiens

<400> 506
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
1 5 10 15

Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	260	265	270

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507

gccaggcagg tgggcctcag gaggtgcctc caggcggcca gtgggcctga 50
ggccccagca agggctaggg tccatctcca gtcccaggac acagcagcgg 100
ccaccatggc cacgcctggg ctccagcagc atcagagcag cccctgtggt 150
tggcagcaaa gttcagcttg gctgggcccc ctgtgagggg cttcgcgcta 200
cgccctgcgg tgtcccgagg gctgaggtct cctcatcttc tccctagcag 250
tggatgagca acccaacggg ggcccgggga ggggaactgg ccccgaggga 300
gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350
gcagccccc ggaccgggga ggcacagggtg gccccacca cccggaggag 400
cagctcctgc ccctgtccgg gggatgactg attctcctcc gccaggccac 450
ccagaggaga aggccacccc gcctggaggc acaggccatg aggggctctc 500
aggaggtgct gctgatgtgg cttctggtgt tggcagtggg cggcacagag 550
cacgcctacc ggcccggccg tagggtgtgt gctgtccggg ctcacgggga 600
ccctgtctcc gagtcttgc tgcagcgtgt gtaccagccc ttctcacca 650
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gactcgtgac tgcccagcgc tccaggctgg actgagcccc tcacgccgcc 1350
ctgcagcccc catgccctg cccaacatgc tgggggtcca gaagccacct 1400
cggggtgact gagcgaagg ccaggcaggg ccttctcct cttcctcctc 1450

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
				260					265					270

Lys Asp Ser

<210> 509
 <211> 1538
 <212> DNA
 <213> Homo sapiens

<400> 509
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 acaggccagg caggtgggcc tcaggaggtg cctccaggcg gccagtgggc 100
 ctgaggcccc agcaagggtt aggggtccatc tccagtcca ggacacagca 150
 gcggccacca tggccacgcc tgggtctcag cagcatcagc agccccagg 200
 accggggagg cacaggtggc ccccaccacc cggaggagca gctcctgccc 250
 ctgtccgggg gatgactgat tctcctccgc caggccaccc agaggagaag 300
 gccaccccg cctggaggcac aggccatgag gggctctcag gaggtgctgc 350
 tgatgtgggt tctggtgttg gcagtgggag gcacagagca cgcctaccgg 400
 cccggccgta ggggtgtgtg tgtccggggt caccggggacc ctgtctccga 450
 gtcgttcgtg cagcgtgtgt accagccctt cctcaccacc tgcgacgggc 500
 accgggcctg cagcacctac cgaaccatct ataggaccgc ctaccgccgc 550
 agccctgggc tggccctgc caggcctgc tacgctgct gccccggctg 600
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 tcctggagga gcagctgggg tcctgctcct gcaagaaaga ctggtgactg 1150
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 aggctcccca gaccctggca tgggatgggc tgggatcttc tctgtgaatc 1350
 caccctggc taccctccacc ctggctaccc caacggcatc ccaaggccag 1400
 gtgggccctc agctgagga aggtacgagc tccctgctgg agcctgggac 1450
 ccatggcaca ggccaggcag cccggaggct ggggtggggcc tcagtggggg 1500
 ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 510
 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
 1 5 10 15
 Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
 110 115 120
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 125 130 135
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

140	145	150
Arg Cys Val Asn Thr Ala Gly Ser Tyr	Trp Cys Gln Cys Trp	Glu
155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys
260	265	270
Lys Asp Ser		

<210> 511
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 511
 tggagcagca atatgccagc c 21

<210> 512
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 512
 ttttcactc ctgtcgggtt gg 22

<210> 513
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 513
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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ggagacagcc tcccggccccg gggaggacaa gtgctgcca cttttggtg 100
ccgacgtgat tccctgggac ggtccgtttc ctgccgtcag ctgccggccg 150
agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200
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ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350
cattttggag caggaattcc aatcatgtct gtgatggtg tgagaaagaa 400
ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450
atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550
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tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800
acatgcaaga tcttccggcc tccccgggcc tcccattgca gcatctgtga 850
caactgtgtg gagcgcttcg accatcactg cccctgggtg ggggaattgtg 900
ttggaaagag gaactaccgc tacttctacc tcttcacact ttctctctcc 950
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ttctagaagt cctcatttgc ttctttacac tctggtccgt cgtgggactg 1100

actggatttc atactttcct cgtggctctc aaccagacaa ccaatgaaga 1150
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atggcaatat tgtgaagaac tgctgtgaag tgctgtgtgg ccccttgccc 1250
cccagtgtgc tggatcgaag gggatatttg ccaactggagg aaagtggaag 1300
tcgacctccc agtactcaag agaccagtag cagcctcttg ccacagagcc 1350
cagccccac agaacacctg aactcaaag agatgccgga ggacagcagc 1400
actcccgaag agatgccacc tccagagccc ccagagccac cacaggaggc 1450
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taattagggc tatgagagat ttcagggtgag aagttaaacc tgagacagag 1550
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caaggcagtg gcagaagatg tcagtcacct ctgataactg gaaaaatggg 1700
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tgggggtcaga agattctcct ggccaccaag tgccagcatt gccacaaat 2000
ccttttagga atgggacagg taccttcac ttgttgtann nnnnnnnnn 2050
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caggaatggc agtaataaaa gtctgcactt tggtcatttc ttttcctcag 2150
aggaagcccg agtgctcact taaacactat cccctcagac tccctgtgtg 2200
aggcctgcag aggccctgaa tgcacaaatg ggaaaccaag gcacagagag 2250
gctctcctct cctctcctct ccccgatgt accctcaaaa aaaaaaaat 2300
gctaaccagt tcttcatta agcctcggct gagtgaggga aagcccagca 2350
ctgctgccct ctggggtaac tcaccctaag gcctcgccc acctctggct 2400
atggtaacca cactgggggc ttcctccaag ccccgctctt ccagcacttc 2450
caccggcaga gtcccagagc cacttcaccc tgggggtggg ctgtggcccc 2500
cagtcagctc tgctcaggac ctgctctatt tcagggaaga agatttatgt 2550

attatatgtg gctatatttc ctagagcacc tgtgttttcc tctttctaag 2600
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<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

<400> 515
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35 40 45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
50 55 60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
65 70 75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
80 85 90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
95 100 105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
110 115 120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
125 130 135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
140 145 150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
155 160 165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
170 175 180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
185 190 195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
200 205 210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
215 220 225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

	230		235		240
Gly Leu Thr Gly	Phe His Thr Phe Leu	Val Ala Leu Asn Gln Thr			
	245	250	255		
Thr Asn Glu Asp	Ile Lys Gly Ser Trp	Thr Gly Lys Asn Arg Val			
	260	265	270		
Gln Asn Pro Tyr	Ser His Gly Asn Ile	Val Lys Asn Cys Cys Glu			
	275	280	285		
Val Leu Cys Gly	Pro Leu Pro Pro Ser	Val Leu Asp Arg Arg Gly			
	290	295	300		
Ile Leu Pro Leu	Glu Glu Ser Gly Ser	Arg Pro Pro Ser Thr Gln			
	305	310	315		
Glu Thr Ser Ser	Ser Leu Leu Pro Gln	Ser Pro Ala Pro Thr Glu			
	320	325	330		
His Leu Asn Ser	Asn Glu Met Pro Glu	Asp Ser Ser Thr Pro Glu			
	335	340	345		
Glu Met Pro Pro	Pro Glu Pro Pro Glu	Pro Pro Gln Glu Ala Ala			
	350	355	360		
Glu Ala Glu Lys					

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 tttggctttg gactctcnc tttctccaca gagcncctcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
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 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

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<223> Synthetic oligonucleotide probe

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200
tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250
aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300
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ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctggtc 400
cttctgagca acacccaaac gcagtacagc atcgagatcc agaactgga 450
tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500
caaagacctc taggggccac ctcatgtgac aagtatctcc caaaattgta 550
gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600
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 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523

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Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
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Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
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Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
				125					130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
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Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

<210> 524
 <211> 503
 <212> DNA
 <213> Homo sapiens

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 gag 503

<210> 525
 <211> 2602
 <212> DNA
 <213> Homo sapiens

<400> 525
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tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150
aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctggtctt 200
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cagcgaaatc cggaccgcat ttgaggaggc cctgggacag ctggtttgga 1450
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Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu	35	40	45
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro	50	55	60
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	125	130	135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu	140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly	170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	215	220	225
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala	230	235	240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu	245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met	260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	275	280	285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	290	295	300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	305	310	315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser			

				320					325					330
Glu	Pro	Val	Val	Val 335	Tyr	Gly	Met	Asp	Tyr 340	Leu	Gln	Gln	Val	Ser 345
Glu	Leu	Ile	Asn	Arg 350	Thr	Glu	Pro	Ser	Ile 355	Leu	Asn	Asn	Tyr	Leu 360
Ile	Trp	Asn	Leu	Val 365	Gln	Lys	Thr	Thr	Ser 370	Ser	Leu	Asp	Arg	Arg 375
Phe	Glu	Ser	Ala	Gln 380	Glu	Lys	Leu	Leu	Glu 385	Thr	Leu	Tyr	Gly	Thr 390
Lys	Lys	Ser	Cys	Val 395	Pro	Arg	Trp	Gln	Thr 400	Cys	Ile	Ser	Asn	Thr 405
Asp	Asp	Ala	Leu	Gly 410	Phe	Ala	Leu	Gly	Ser 415	Leu	Phe	Val	Lys	Ala 420
Thr	Phe	Asp	Arg	Gln 425	Ser	Lys	Glu	Ile	Ala 430	Glu	Gly	Met	Ile	Ser 435
Glu	Ile	Arg	Thr	Ala 440	Phe	Glu	Glu	Ala	Leu 445	Gly	Gln	Leu	Val	Trp 450
Met	Asp	Glu	Lys	Thr 455	Arg	Gln	Ala	Ala	Lys 460	Glu	Lys	Ala	Asp	Ala 465
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Phe	Phe	Gln	Asn	Met 500	Leu	Asn	Leu	Tyr	Asn 505	Phe	Ser	Ala	Lys	Val 510
Met	Ala	Asp	Gln	Leu 515	Arg	Lys	Pro	Pro	Ser 520	Arg	Asp	Gln	Trp	Ser 525
Met	Thr	Pro	Gln	Thr 530	Val	Asn	Ala	Tyr	Tyr 535	Leu	Pro	Thr	Lys	Asn 540
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Arg	Asn	His	Pro	Lys 560	Ala	Leu	Asn	Phe	Gly 565	Gly	Ile	Gly	Val	Val 570
Met	Gly	His	Glu	Leu 575	Thr	His	Ala	Phe	Asp 580	Asp	Gln	Gly	Arg	Glu 585
Tyr	Asp	Lys	Glu	Gly 590	Asn	Leu	Arg	Pro	Trp 595	Trp	Gln	Asn	Glu	Ser 600
Leu	Ala	Ala	Phe	Arg 605	Asn	His	Thr	Ala	Cys 610	Met	Glu	Glu	Gln	Tyr 615

Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr	620	625	630
Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr	635	640	645
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln	650	655	660
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly	665	670	675
Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His	680	685	690
Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val	695	700	705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly	710	715	720
Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val	725	730	735

Trp

<210> 527
 <211> 4308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1478, 3978, 4057-4058, 4070
 <223> unknown base

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<210> 612
<211> 352
<212> PRT
<213> Homo Sapien

<400> 612
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35 40 45
Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
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Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
65 70 75
Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
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Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
95 100 105
Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
110 115 120
Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
125 130 135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
140 145 150
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
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Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
170 175 180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln
185 190 195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
200 205 210
Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
215 220 225
Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

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Ile Arg Cys Glu	Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp			
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Tyr Lys Gly Glu	Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile			
	260	265			270
Ile Gln Asn Phe	Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val			
	275	280			285
Thr Gln Glu His	Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys			
	290	295			300
Leu Gly Thr Thr	Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr			
	305	310			315
Ala Gln Tyr Gly	Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys			
	320	325			330
Trp Tyr Leu Val	Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr			
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Leu Lys Asn Ala	Ile Leu Gln				
	350				

<210> 613
 <211> 1797
 <212> DNA
 <213> Homo Sapien

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<210> 614
<211> 520
<212> PRT
<213> Homo Sapien

<400> 614
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Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
20 25 30

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	335		340		345
Gly Leu Lys Gly	Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln			
	350		355		360
Gly Arg Lys Gly	Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys			
	365		370		375
Gly Glu Gln Gly	Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro			
	380		385		390
Gly Gln Ala Gly	Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser			
	395		400		405
Gly Glu Gln Gly	Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn			
	410		415		420
Ser Val Ser Val	Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala			
	425		430		435
Glu Val Tyr Tyr	Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu			
	440		445		450
Trp Gln Asn Ser	Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr			
	455		460		465
Ser Lys Gly Arg	Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln			
	470		475		480
Ile Trp Leu Asp	Asn Val Gln Cys Arg	Gly Thr Glu Ser Thr Leu			
	485		490		495
Trp Ser Cys Thr	Lys Asn Ser Trp Gly	His His Asp Cys Ser His			
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Glu Glu Asp Ala	Gly Val Glu Cys Ser	Val			
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<210> 615

<211> 647

<212> DNA

<213> Homo Sapien

<400> 615

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<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
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 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
 50 55 60
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
 65 70 75
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
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 Phe Val Ile Pro Cys Asn Asn Gln
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<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

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<210> 618
<211> 750
<212> PRT
<213> Homo Sapien

<400> 618
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Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
35 40 45
Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
50 55 60
Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
65 70 75
Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
80 85 90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	95	100	105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	110	115	120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	125	130	135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	140	145	150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	215	220	225
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Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	245	250	255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	260	265	270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	320	325	330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	335	340	345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	350	355	360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	365	370	375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser			

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Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser	
				410					415					420	
Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala	
				425					430					435	
Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	Tyr	Ile	
				440					445					450	
Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	Asp	
				455					460					465	
Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu	
				470					475					480	
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	
				485					490					495	
Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	
				500					505					510	
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	
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Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	
				590					595					600	
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	
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Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys	
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Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val	
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Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
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Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
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<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

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<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

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<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623
<211> 25
<212> DNA
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